1 TGGCAGTGGG CGGCGTAGAG CACTGCAGCA GCAATGACGG AGGGCACGTG 51 TCTGCGGCGC CGAGGGGGCC CCTACAAGAC CGAGCCCGCC ACCGACCTCG 101 GCCGCTGGCG ACTCAACTGC GAGAGGGGCC GGCAGACGTG GACCTACCTG 151 CAGGACGAGC GCGCCGGCCG CGAGCAGACC GGCCTGGAAG CCTACGCCCT 201 GGGGCTGGAC ACCAAGAATT ACTTTAAGGA CTTGCCCAAA GCCCACACCG 251 CCTTTGAGGG GGCTCTGAAC GGGATGACAT TTTACGTGGG GCTGCAGGCT 301 GAGGATGGC ACTGGACGGG TGATTATGGT GGCCCACTTT TCCTCCTGCC 351 AGGCCTCCTG ATCACTTGCC ACGTGGCACG CATCCCTCTG CCAGCCGGAT 401 ACAGAGAAGA GATTGTGCGG TACCTGCGGC ACATTGAGGA TAAGTCCACC 451 GTGTTTGGGA CTGCGCTCAA CTATGTGTCT CTCAGAATTC TGGGTGTTGG 501 GCCTGACGAT CCTGACCTGG TACGAGCCCG GAACATTCTT CACAAGAAAG 551 GTGGTGCTGT GGCCATCCCC TCCTGGGGGA AGTTCTGGCT GGCTGTCCTG 601 AATGTTTACA GCTGGGAAGG CCTCAATACC CTGTTCCCAG AGATGTGGCT 651 GTTTCCTGAC TGGGCACCGG CACACCCCTC CACACTCTGG TGCCACTGCC 701 GGCAGGTGTA CCTGCCCATG AGCTACTGCT ACGCCGTTCG GCTGAGTGCC 751 GCGGAAGACC CGCTGGTCCA GAGCCTCCGC CAGGAGCTCT ATGTGGAGGA 801 CTTCGCCAGC ATTGACTGGC TGGCGCAGAG GAACAACGTG GCCCCCGACG 851 AGCTGTACAC GCCGCACAGC TGGCTGCTCC GCGTGGTATA TGCGCTCCTC 901 AACCTGTATG AGCACCACCA CAGTGCCCAC CTGCGGCAGC GGGCCGTGCA 951 GAAGCTGTAT GAACACATTG TGGCCGACGA CCGATTCACC AAGAGCATCA 1001 GCATCGGCCC GATCTCGAAA ACCATCAACA TGCTTGTGCG CTGGTATGTG 1051 GACGGGCCCG CCTCCACTGC CTTCCAGGAG CATGTCTCCA GAATCCCGGA 1101 CTATCTCTGG ATGGGCCTTG ACGGCATGAA AATGCAGGGC ACCAACGGCT 1151 CACAGATCTG GGACACCGCA TTCGCCATCC AGGCTCTGCT TGAGGCGGGC 1201 GGGCACCACA GGCCCGAGTT TTCGTCCTGC CTGCAGAAGG CTCATGAGTT 1251 CCTGAGGCTC TCACAGGTCC CAGATAACCC TCCCGACTAC CAGAAGTACT 1301 ACCGCCAGAT GCGCAAGGGT GGCTTCTCCT TCAGTACGCT GGACTGCGGC 1351 TGGATCGTTT CTGACTGCAC GGCTGAGGCC TTGAAGGCTG TGCTGCTCCT 1401 GCAGGAGAG TGTCCCCATG TCACCGAGCA CATCCCCAGA GAACGGCTCT 1451 GCGATGCTGT GGCTGTGCTG CTGAACATGA GAAATCCAGA TGGAGGGTTC 1501 GCCACCTATG AGACCAAGCG TGGGGGGCAC TTGCTGGAGC TGCTGAACCC 1551 CTCGGAGGTC TTCGGGGACA TCATGATTGA CTACACCTAT GTGGAGTGCA 1601 CCTCAGCCGT GATGCAGGCG CTTAAGTATT TCCACAAGCG TTTCCCGGAG 1651 CACAGGGCAG CGGAGATCCG GGAGACCCTC ACGCAGGGCT TAGAGTTCTG 1701 TCGGCGGCAG CAGAGGCCCG ATGGCTCCTG GGAAGGCTCC TGGGGAGTTT 1751 GCTTCACCTA CGGCACCTGG TTTGGCCTGG AGGCCTTCGC CTGTATGGGG 1801 CAGACCTACC GAGATGGGAC TGCCTGTGCA GAGGTCTCCC GGGCCTGTGA 1851 CTTCCTGCTG TCCCGGCAGA TGGCAGACGG AGGCTGGGGG GAGGACTTTG 1901 AGTCCTGCGA GGAGCGGCGT TATGTGCAGA GTGCCCAGTC CCAGATCCAC 1951 AACACATGCT GGGCCATGAT GGGGCTGATG GCCGTTCGGC ATCCTGACAT 2001 CGAGGCCCAG GAGAGAGGAG TCCGGTGTCT ACTTGAGAAA CAGCTCCCCA 2051 ATGGCGACTG GCCGCAGGAA AACATTGCTG GGGTCTTCAA CAAGTCCTGT 2101 GCCATCTCCT ACACGAGCTA CAGGAACATC TTCCCCATCT GGGCCCTCGG 2151 CCGCTTCTCC CAGCTGTACC CTGAGAGAGC CCTTGCTGGC CACCCCTGAG 2201 AACATGCCTA CCTGCTGGGT GCCGTCTGTG CGTTCCAGTG AGGCCAAGGG 2251 GTCCTGGCCG GGTTGGGGAG CCCTCCCATA ACCCTGTCTT GGGCTCCAAC 2301 CCCTCAACCT CTATCTCATA GATGTGAATC TGGGGGCCAG GCTGGAGGCA 2351 GGGATGGGGA CAGGGTGGGT GGCTTAGACT CTTGATTTTT ACTGTAGGTT 2401 CATTTCTGAA AGTAGCTTGT CGGGCTTGGG TGAGGAAGGG GGCACAGGAG 2451 CCGTGACCCC TGAGGAGGCA CAGCGCCTTC TGCCACCTCT GGGCACGGCC 2501 TCAAGGTAGT GAGGCTAGGA GGTTTTTTCT GACCAATAGC TGAGTTCTTG 2551 GGAGAGGAGC AGCTGTGCCT GTGTGATTCC TTAGTGTCGA GTGGGCTCTG 2601 GGCTGGGGTC GGCCCTGGGC AGGCTTCTCC TGCACCTTTT GTCTGCTGGG 2651 CTGAGGGACA CGAGGGCAAC CCTGTGACAA TGGCAGGTAG TGTGCATCCG 2701 TGAATAGCCC AGTGCGGGGG TTGCTCATGG AGCATCCTGA GGCCGTGCAG 2751 CAGGGAGCCC CATGCCCCTG GGTCGTGAGC TTGCCTGCGT ATGGGGTGGT 2801 GTCATGGAGC CTCATGCCCC TGGGTCGTGA GCTCGCCTGA GTATGGGGTG 2851 GTGTCATGGA GCCGCATACC CCTGGGTTGT GAGCTCGCCT GCATATGCAG 2901 GGTCTGTCAT GGAACATCCC AAGTCTGTGC AGCAGGGAGC CCCATGCCCC 2951 TGGGACATGA ACCCACCTGC GTGGAATGCT GTTTGTGAGG TGTCTACAGG 3001 GTTTATAGTA GTCTTGTGGA CACAGAAATG CACAGGGGAC ACTTACGGAC 3051 ACAGAAATGC ACAGGGGAGG CCGAGCATAA CCAGGGGTGA GGGGCAGGCA 3101 GCAGTTGTAG TTACTGCCGC GGGGCACTGC TATGTGCAGG GACAGCCAGC

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3151 GCCCAGCCCA TCACCACTCC CTGGGCTGGC TGGCAGGTAT GGCACCCTGG
3201 GAGCCCGGCA TATACCCAGG GCACCCCTAC GGCTGCCGCC AGTCTCATGC
3251 CCAGGTGGGT GCTCTGGGCT GGAGCGAGGG CCAGGTTTTG GGCCGAGGCT
3301 TCCCCAGGCA ATCCTGTGAG CTCCCTTCTA GCCTCTGACC CAGTCTGGTC
3351 TGGCTTGCAT GGATGTAGGG CTTGGGGTGG GAAGTTCAGG TCCTGGCTTT
3401 GCCTTTGCCT GATGTGGATG AGCAGCTCAC ATGCTCAGGG CCACCTGAGA
3451 CTGTCACTGC TCTCCCCTGG CTACTGGGAG GAGTCACTGA GAGCTTCGTT
3501 ACCCCTGCTG CCTTGCCCAG GGCACACCCT ATACCTCCTC ATCTGCTCTT
3551 CCCCTCCTG CCGCCTTCTG GGCAGGTAGC AGTCCCTGGC CTCTCCCCCT
3601 GGCTGATCAC TCTCCCTCAG GCAGTGGAGA TCTGCGTCTG GACACCCTCA
3651 GATCCTGTCA TTGCCTGCCC AGAGTCCTTC AGGGGCACCC CTCTGCCTTG
3701 GTGTGCGGTC CAGGGCTCTC ACCCAGGTGC CGCACCCTCT GGGGTCTTCT
3751 GTCCAGCTCC CTTGCCCCAT GTGCTGTCAC TGACTCTCCT TGGGACTCGC
3801 CTGCCTGCTC AGAGCCCTGC AGGGCTTGGT CAGCTGCCTG TTCAGTGTCA
3851 ACACTTCCCT GCACATCTTA AAACTGGGCT TTATTTTCGC TGAAGGAACT
3901 GTGTTGGGAC CCTTGACATC TGTCAGGTTT GCACATGCTG TTTTTTTTTC
3951 TCAGCCCACG TGTTCTCCCC CACGTGGGGT AGCAGCAGGA CAGACAGTGA
4001 ATCACAGAGT CTGCCCTGAG CAGAGGCTGC TGTCCCTGGG ACTCCTAGCC
4101 TTTATACTGA AAATGTTACT GAAAGTCACT TTTATGAGCA TCTGCCTTAA
4151 TAAACAGACA TTGATTCCCT TAAAAAAAA AAAAAAAAA AAAAAAAAA
```

FEATURES:

5'UTR: 1-33 Start Codon: 34 Stop Codon: 2197 3'UTR: 2200

Homologous proteins: Top 10 BLAST Hits

TOP TO BLAST HILS		
	Score	E
CRA 18000005000949 /altid=gi 4505027 /def=ref NP_002331.1 lano	1530	0.0
CRA 18000005227733 /altid=gi 4808278 /def=emb CAB42828.1 (AJ23	1524	0.0
CRA 18000005013642 /altid=gi 1098635 /def=gb AAA91023.1 (U3135		0.0
CRA 18000004977416 /altid=gi 1352388 /def=sp P48450 ERG7_RAT LA	1305	0.0
CRA 18000005002424 /altid=gi 984145 /def=emb CAA61078.1 (X8780		0.0
CRA 100000004433519 /altid=gi 8886139 /def=gb AAF80384.1 AF1599		0.0
CRA 335001098658178 /altid=gi 11279144 /def=pir T48782 lanoste		e-173
CRA 18000005223063 /altid=gi 4589852 /def=dbj BAA76902.1 (AB02		e-173
CRA 18000005171896 /altid=gi 3688598 /def=dbj BAA33460.1 (AB00		e-172
CRA 1000682333668 /altid=gi 6045133 /def=dbj BAA85266.1 (AB033	605	e-172

BLAST dbEST hits:

	score	Ľ
gi 10993792 /dataset=dbest /taxon=96	1538	0.0
gi 10159427 /dataset=dbest /taxon=96	1358	0.0
gi 9340844 /dataset=dbest /taxon=960	1108	0.0
gi 11251687 /dataset=dbest /taxon=96	1065	0.0
gi 11258382 /dataset=dbest /taxon=96	995	0.0
gi 10322370 /dataset=dbest /taxon=96	910	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|10993792 teratocarcinoma

gi|10159427 ovary gi|9340844 uterus gi|11251687 muscle

gi 11258382 brain

gi 10322370 colon

From tissue screening panels:

hippocampus

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1 MTEGTCLRRR GGPYKTEPAT DLGRWRLNCE RGRQTWTYLQ DERAGREQTG
51 LEAYALGLDT KNYFKDLPKA HTAFEGALNG MTFYVGLQAE DGHWTGDYGG
101 PLFLLPGLLI TCHVARIPLP AGYREEIVRY LRHIEDKSTV FGTALNYVSL
151 RILGVGPDDP DLVRARNILH KKGGAVAIPS WGKFWLAVLN VYSWEGLNTL
201 FPEMWLFPDW APAHPSTLWC HCRQVYLPMS YCYAVRLSAA EDPLVQSLRQ
251 ELYVEDFASI DWLAQRNNVA PDELYTPHSW LLRVVYALLN LYEHHHSAHL
301 RQRAVQKLYE HIVADDRFTK SISIGPISKT INMLVRWYVD GPASTAFQEH
351 VSRIPDYLWM GLDGMKMQGT NGSQIWDTAF AIQALLEAGG HHRPEFSSCL
401 QKAHEFLRLS QVPDNPPDYQ KYYRQMRKGG FSFSTLDCGW IVSDCTAEAL
451 KAVLLLQEKC PHVTEHIPRE RLCDAVAVLL NMRNPDGGFA TYETKRGGHL
501 LELLNPSEVF GDIMIDYTYV ECTSAVMQAL KYFHKRFPEH RAAEIRETLT
551 QGLEFCRQQ RADGSWEGSW GVCFTYGTWF GLEAFACMGQ TYRDGTACAE
601 VSRACDFLLS RQMADGGWGE DFESCEERRY VQSAQSQIHN TCWAMMGLMA
651 VRHPDIEAQE RGVRCLLEKQ LPNGDWPQEN IAGVFNKSCA ISYTSYRNIF
```

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION N-glycosylation site

Number of matches: 2 1 371-374 NGSQ 2 686-689 NKSC

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

Number of matches: 5
1 149-151 SLR
2 247-249 SLR
3 149-151 SLR
4 247-249 SLR
5 494-496 TKR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

[4] PDOC00008 PS00008 MYRISTYL N-myristoylation site

Number of	matches:	11
1	76-81	GALNGM
2	107-112	GLLITC
3	142-147	GTALNY
4	173-178	GGAVAI
5	369-374	GTNGSQ
6	487-492	GGFATY
7	552-557	GLEFCR
8	564-569	GSWEGS
9	571-576	GVCFTY
10	577-582	GTWFGL
11	595-600	GTACAE

[5] PDOC00825 PS01074 TERPENE_SYNTHASES Terpene synthases signature

563-577 DGSWEGSWGVCFTYG

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	95	115	1.321	Certain
2	173	193	0.944	Putative
3	569	589	1.311	Certain

BLAST Alignment to Top Hit: >CRA 18000005000949 /altid=gi 4505027 /def=ref NP_002331.1 lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase); Lanosterol synthase; human lanosterol synthase [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=732 Length = 732Score = 1530 bits (3917), Expect = 0.0Identities = 720/732 (98%), Positives = 721/732 (98%), Gaps = 11/732 (1%) ${\tt MTEGTCLRRRGGPYKTEPATDLGRWRLNCERGRQTWTYLQDERAGREQTGLEAYALGLDT~60}$ Query: 1 ${\tt MTEGTCLRRRGGPYKTEPATDLGRWRLNCERGRQTWTYLQDERAGREQTGLEAYALGLDT}$ Sbjct: 1 MTEGTCLRRRGGPYKTEPATDLGRWRLNCERGRQTWTYLQDERAGREQTGLEAYALGLDT 60 Query: 61 KNYFKDLPKAHTAFEGALNGMTFYVGLQAEDGHWTGDYGGPLFLLPGLLITCHVARIPLP 120 KNYFKDLPKAHTAFEGALNGMTFYVGLQAEDGHWTGDYGGPLFLLPGLLITCHVARIPLP Sbjct: 61 KNYFKDLPKAHTAFEGALNGMTFYVGLQAEDGHWTGDYGGPLFLLPGLLITCHVARIPLP 120 Query: 121 AGYREEIVRYLR------HIEDKSTVFGTALNYVSLRILGVGPDDPDLVRARNIL 169 AGYREEIVRYLR HIEDKSTVFGTALNYVSLRILGVGPDDPDLVRARNIL Sbjct: 121 AGYREEIVRYLRSVQLPDGGWGLHIEDKSTVFGTALNYVSLRILGVGPDDPDLVRARNIL 180 Query: 170 HKKGGAVAIPSWGKFWLAVLNVYSWEGLNTLFPEMWLFPDWAPAHPSTLWCHCRQVYLPM 229 HKKGGAVAIPSWGKFWLAVLNVYSWEGLNTLFPEMWLFPDWAPAHPSTLWCHCRQVYLPM Sbjct: 181 HKKGGAVAIPSWGKFWLAVLNVYSWEGLNTLFPEMWLFPDWAPAHPSTLWCHCRQVYLPM 240 Query: 230 SYCYAVRLSAAEDPLVQSLRQELYVEDFASIDWLAQRNNVAPDELYTPHSWLLRVVYALL 289 SYCYAVRLSAAEDPLVQSLRQELYVEDFASIDWLAQRNNVAPDELYTPHSWLLRVVYALL Sbjct: 241 SYCYAVRLSAAEDPLVQSLRQELYVEDFASIDWLAQRNNVAPDELYTPHSWLLRVVYALL 300 Query: 290 NLYEHHHSAHLRQRAVQKLYEHIVADDRFTKSISIGPISKTINMLVRWYVDGPASTAFQE 349 NLYEHHHSAHLRQRAVQKLYEHIVADDRFTKSISIGPISKTINMLVRWYVDGPASTAFQE Sbjct: 301 NLYEHHHSAHLRQRAVQKLYEHIVADDRFTKSISIGPISKTINMLVRWYVDGPASTAFQE 360 Query: 350 HVSRIPDYLWMGLDGMKMQGTNGSQIWDTAFAIQALLEAGGHHRPEFSSCLQKAHEFLRL 409 HVSRIPDYLWMGLDGMKMQGTNGSQIWDTAFAIQALLEAGGHHRPEFSSCLQKAHEFLRL Sbjct: 361 HVSRIPDYLWMGLDGMKMQGTNGSQIWDTAFAIQALLEAGGHHRPEFSSCLQKAHEFLRL 420 Query: 410 SQVPDNPPDYQKYYRQMRKGGFSFSTLDCGWIVSDCTAEALKAVLLLQEKCPHVTEHIPR 469 SQVPDNPPDYQKYYRQMRKGGFSFSTLDCGWIVSDCTAEALKAVLLLOEKCPHVTEHIPR Sbjct: 421 SQVPDNPPDYQKYYRQMRKGGFSFSTLDCGWIVSDCTAEALKAVLLLQEKCPHVTEHIPR 480 Query: 470 ERLCDAVAVLLNMRNPDGGFATYETKRGGHLLELLNPSEVFGDIMIDYTYVECTSAVMQA 529 ERLCDAVAVLLNMRNPDGGFATYETKRGGHLLELLNPSEVFGDIMIDYTYVECTSAVMQA Sbjct: 481 ERLCDAVAVLLNMRNPDGGFATYETKRGGHLLELLNPSEVFGDIMIDYTYVECTSAVMQA 540 Query: 530 LKYFHKRFPEHRAAEIRETLTQGLEFCRRQQRADGSWEGSWGVCFTYGTWFGLEAFACMG 589 LKYFHKRFPEHRAAEIRETLTQGLEFCRRQQRADGSWEGSWGVCFTYGTWFGLEAFACMG Sbjct: 541 LKYFHKRFPEHRAAEIRETLTQGLEFCRRQQRADGSWEGSWGVCFTYGTWFGLEAFACMG 600 Query: 590 QTYRDGTACAEVSRACDFLLSRQMADGGWGEDFESCEERRYVQSAQSQIHNTCWAMMGLM 649 QTYRDGTACAEVSRACDFLLSRQMADGGWGEDFESCEERRY+QSAQSQIHNTCWAMMGLM Sbjct: 601 QTYRDGTACAEVSRACDFLLSRQMADGGWGEDFESCEERRYLQSAQSQIHNTCWAMMGLM 660 Query: 650 AVRHPDIEAQERGVRCLLEKQLPNGDWPQENIAGVFNKSCAISYTSYRNIFPIWALGRFS 709 AVRHPDIEAQERGVRCLLEKQLPNGDWPQENIAGVFNKSCAISYTSYRNIFPIWALGRFS Sbjct: 661 AVRHPDIEAQERGVRCLLEKQLPNGDWPQENIAGVFNKSCAISYTSYRNIFPIWALGRFS 720 Query: 710 QLYPERALAGHP 721 QLYPERALAGHP Sbjct: 721 QLYPERALAGHP 732 (SEQ ID NO:4)

FIGURE 3C

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00432	Prenyltransferase and squalene oxidase repea	83.9	1.7e-22	3

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00432	1/3	133	154	23	45 .	.] 6.6	3.8
PF00432	2/3	547	589	1	45	[] 40.1	8e-10
PF00432	3/3	599	647	1	45	[] 39.4	1.3e-09

1 TCATGACTGC CCCTAGAAGC TTAACTGTGT CAATTCTCAG ACGTAGTTTA 51 CAGCTTTTC TTTTCTTCA GACATTAAAA AGAGCGGATT ATTTTACTCA 101 TAAAAAGTCC AGTCCATTAA GATATCAAAA CTCAAACTCT TATCCAGTTG 151 AAACCTCTTC CCTCACCTAG CTTTGCCAGG TTCAGTGTGA GATTCCATCC 201 AGGCTGAAGC CCCTTATCCC TATTCTTCAT GTTTCTACAT GGAGGAACTT 251 ACCTGGAGAA AAACTTCCAG CCTCTTTCTG CTTCCAGAGA AGTAGAGTGA 301 CTCATTTGAT TGAATTTCAG AGAACAGATA GGGTGGAGTG TGCTCAGGCT 351 CCTCTGGGTA CTCTTTCTGG GGTCTGTGGG TTGACTGGAG GGGTGTCTTC 401 TGGTGGCAC TCAATTGCAT AGTGCTTGGT GAGGCAGTTT CATGGCCTAG 451 AGGCTGGGGG ATATGTTTGT CTGACTTACG GGTGATTTAG TAGCTTGCCC 501 TCTTGCTTGC AGATTTAAGC CTTGTCCTTC AAGCTAGGTT TTTAATTTGT 551 GGCAAAGCTG ATATTTTGAT ACCCACCCAT CTTATTGCTG TGTCTTTTTC 601 ATCCGTTTCT GAACTGGGAT AGGAAGAGGT GATTATCCTT GATTGTCTAA 651 AACCCCGCTA TTCCACTGTG GGGAAGGTGC CTGTGGGTAT TCTTTTGTCC 701 ACTCTCTCT CCAACTTTCT CCTCCGGCTT GCTGTGGCTC ACCGCCCCTT 751 CGAAGTTAGG CTGGGGGTAG GAATTGAGGA GTGGGTGCCG AAATGCTCAC 801 TAGGCTGGGG CAGTTGTAAC TGGATGTCAG GGCTTCTGTG GGCCAGGTGA 851 AGACATGCTG GGGTCTTCTG TGGGTCCTTG ACCTGACTTA GGGACCACTG 901 GCTGCAGCCT CCAGACGTCA GCCATGTTTC CAACAGTCAG ACGCCCCCTG 951 CCCTGTTGCG CCCGGCTGTC CCTTCCAAGT TCGGTCACTC GCTCTGCCTC 1001 CATCTTCCTC TTCCCTCTGC TGCTAAGGCT TTTCACCTTT AATTTCTCCT 1051 GGGGCCACCC CCAACTCCAG CGACCCCGTG AGCAGCTGAG GCTCTACCGC 1101 GCTCGGTCCT GGCCAGCGAC GCAGCCCTTC CCTGGCGGGG CTCCAGGGCT 1151 TCTGGCCCCT GTGGTCCGCC AGGTGTGGGG GCCCACGGCC TCACCGCGCC 1201 TACCCCACTC CCCCCGGCGA AGCTACGCGG CGCTCAGCTT CCCAGGGACG 1251 CCGGCGGCGC CCTCGGCTCC TCCGCTCCGC CCCGCCCTCC CCCTGGTCTC 1301 GCACTGGAGC CGACGGCCCG CGCCCACCTC ACCTCAGGGC GGCCTCCCGC 1351 CCCCACCCC GGCCCGGCG TCCGGGCAAA TCCTGCAGCG CGAGAGCAAT 1401 TCCTGCCAC CCGACCTTCG CACTCGCTGT CGCTCGCTCG AGCCTCGCTC 1451 CCCACGTCCT TCCTTCCGAC CCGCGGCTGG ACCCTCCTCA CAAATTTCTC 1501 AGAGAGGCTC ACCTCAAAGC GCGCGCACG AGGCCGGGCT CCCGGGACGC 1551 AAGCCTCTAG AGGGCGCGCG AGAGGCCCCG CCCCGCCCT TCGGCCCCAC 1601 CCACCAGCCC CGCCCCCACC CGCACCCACC AGGCCCCGCC CCCACCTCCC 1651 CACCCACCAG CCCCGCCCCC ACCTCCCCAC CCACCAGCCC CGCCCCTCAT 1751 ACCATCCCCG CTCCCTCAGG CCCCGCCCCA CGCCGCATGG GGCACCAAGC 1801 GCTCCACCAC TGTGGTCGCC TGGCACACCC CGGGGTCACG CTCGCGGCGC 1851 TCTGATTGGT TGCGTGGGCG TCGGCCCACC TAAGCCTGAG CGCCTGCCGA 1901 GGCCTGCGCC TGCGTAGTGC GCGCGGAGGG GGCGGAGGGG GCGGGAGGGG 1951 CGGGAGGGC GGGGCTGGGC GGCAGGTCCC GGGTGCGGAC ATCTGGCAGC 2001 TGGCAGTGGG CGGCGTAGAG CACTGCAGCA GCAATGACGG AGGGCACGTG 2051 AGTCCCCTCG CCCCGGGCTC CTGACGAATG CGGGGTGGTC CTAGGTGCTG 2151 CTGGGTCGCT GATGGCCGGT GGTCCTCAGG TGTCTGCGGC GCCGAGGGGG 2201 CCCCTACAAG ACCGAGCCG CCACCGACCT CGGCCGCTGG CGACTCAACT 2251 GCGAGAGGG CCGGCAGACG TGGACCTACC TGCAGGACGA GCGCGCCGGC 2301 CGCGAGCAGA CCGGCCTGGA AGCCTACGCC CTGGGGCTGG ACACCGTAAG 2351 TTGCTTCCGC GGAGCGTCAG CGAGCTCGGG ACCCTGAGGG GTGAGCCGTG 2401 AGGAGCACGT TTTCTCTCAG AAAGGCGGGT GGGAGGACCC GGCCAGCGAC 2451 GCCCATCCC AAGGCGAGCG CCCACGGGAA CTGCGTTCGC GGGCCCCTCC 2501 GCTTCAGCCC CTTCATCTCT AAACCACGCA TAGGAGACTC CTAATGTTTT 2551 ATTTTTAGC ACCTTATTTT GAGATAATTT TTGACTTATA GGAGAGTTGC 2601 AAAGATAGTT GTAACTTTGT TTTTATTCAC AAAAAGTGTT TGGATCCACT 2651 GTCTTAGTTG TGTGCATTGT AAGAGATTTT GGTCGTCAGA GTCTGCAGTG 2701 TAAACAGGGT CTCCTGCCGA GCCCCGGCCA CCGAGGGAAA GGCTGTGCCG 2751 CCCCTTGGGC CCTCTTTGAG AGGCCCGAGT CCCAGGCCCA GGTCGGCACC 2801 CGTGCCCCAC CCTACAGTCT GGGTGCCTGG TTTATTCCAG ACATCTTGGA 2851 GAAGTTGTGA AGAATACATG ACTGGCAAAT AAAGCAACGA AAATGTGCAG 2901 CTGTTCTTTT ACTTTGCTGA GGTGTGATGC TCTCATCAAA GAGTTTCAGA 2951 CTTTTGATGG AAACAGCTGA AACTTTTAAA GTAATTTACA TTCACTGTTT 3001 TGACTTGGGC TGTATGTGAA GAGGGTTCCT CTGGCCGGGC AACAGTCCCG 3051 TCAGCTATCT CTTTTTTTT TTTTCGATCT CTTTGCAGAA GAATTACTTT 3101 AAGGACTTGC CCAAAGCCCA CACCGCCTTT GAGGGGGCTC TGAACGGGAT 3151 GACATTTTAC GTGGGGCTGC AGGCTGAGGA TGGGCACTGG ACGGGTGATT 3201 ATGGTGGCCC ACTTTTCCTC CTGCCAGGTA GGAGTATGCT GCCCCAGCCT 3251 GATGGTATGG CCACCCTGGA TCACCCTTGG GATCCTGGCC CAGCCTGGTC 3301 TAGGGTTTTG ATGAAGCAGG TGAAAATCCA GGGGCTCACA AGAAAAGGGC 3351 TGGCAAACTC TGCCCTATGT CAGAGTCGTC CTGCTATTGG TCTAGGGGAT 3401 CAGCTAGCCT TGCCAGTGTA GGGTGACAGG CTCTCTGATA AGAGAAGCAA 3451 GTGGTTCTCT AGGGCTCTGT GTTGCCTTGA GGGAGGAGGA AGGTGGGCTT 3501 TGAAGTCTCA GTACAGGATG GGATGGACAT TCCAGGTGGA AGGCCCAGCC 3551 TATGCCAAGG GGCTGTAGGT GGGCAGAGTG GTGGGTGGGG AGCTGATATC 3601 TGCTGTGAAC TTCCTCGGGG CTATTGCAGG AGAGCTTCAG GTTCAGGCTG 3651 GTGAGTAGGA GGAGCATAGC AGTTGGACTG CCTGGGTATT GAACTGATTT 3701 GGCTACACAA GACTATTTTG CATCCTGGGA GTGTTTCTCT ACAGAAATCC 3751 TCAGCCTTGT AAAATGGGAA ATTCCCTCCT ATGAATTTAT GCAATAGGAC 3801 TTTTTTCCCT AGTGACTTGT AATCACATTG TTTCAATGAC GTGAATTCCT 3851 ACATAAATAG GTTTTGTTTC TGTGATAACT CTTACTGATA CATCATTTTC 3901 TTTTACTACG CTGACTTTGT AATAGATAGA AAGTCCTTAT ATACCTTTGT 3951 TGCCTTTCTT TTTAAAACAT CTCTTACCTG TGTCTATTCA TTTACTCATC 4001 CAAATTGCCT TTATCCTGAT TTTGTCCCAG ACTTGAAATG AAGTTGCAAT 4051 AGGCTTATAT GTTAGTTTGG GAAGAGTTGG CCTTTAACGT TAAAAACAGT 4101 TCCATGGTGT TTACTGTAGG CCAAGCCCTG CTCAAGGCCT GTTCTTCTTT 4151 TAGTCCTTAG AATAAGCCTA ATGAGATACA TTAGAAAGCT GAGGCACATT 4201 TATTCCAGGT AACCAGACTA GCAGGAGGAG CACTGGGATC CCCATCTCTG 4251 CTTTGACTTC TAGCCCTGCT GCCACCTGGA CTGTACAGCA TTGAGTTTTT 4301 CTGTCCTGGG ATTTGAGGGC CTGTCCTTAG GGGAAGTCAA GGTGCTCTTC 4351 TTCCCTTGGC CCCATCAGGG CCTGTTTAGA CTGTTCTCAG GGCTCGTGGT 4401 AAGGCAATGA CATAGAGTTG GTCAGGAGAT GGGTCAGCCC CACTTTGCCT 4451 CTGTAGCCTG ACCTGTGACA GGATTGGAAT CAGGTTTGGT CATGTGCACA 4501 GTGTCAGGCA TGCAGTGGTG CTTGGTCAGT GGGGATTACT GTGTTGTTTG 4551 TTCTTGCTGC TTTGGCTCTG GGCTTAGCTG GCTGGGACCC TTCCTGTGGG 4601 CTGGCTGTGA GTTGGAGTTT TTTTGTATTT TTTTTTTTT TTTGAGACAG 4651 CGTTCGCTCT TGTTCCCCAG GCTGGAGTGC AATGGCACAA TTTTGGCTCG 4701 TTGCAGCCTC TGCCTCCTGG GTGCAAGTGA TTCTCCTGCC TCAGCCTCCT 4751 GTAGGGTCCA GCCCCACAGG GTCGGTAGGT TTTTCTCCCT GTGTGCGGAG 4851 CAGCTGGGCC CCGGGGGACC ACTACCACCA AGACGTGGAA ACCGGTAGTG 4901 GCCCTGAATG CCAGGCTGCG CTGATATTTA TTGGATACAA GACAAAGGGG 4951 CAGGGTAAGG AGTGTGAGCC ATCTCCAATG ATAGGTAAGG TCACATGGGT 5001 CACGTGTCCA CTGGACAGTG GGCCCTTCCC TGCCTGGCAG CCGAGGCAGA 5051 GAGTGGGAGA GAGAGAGAG GAGACAGCTT ATGCCATTAT TTCTGCATAT 5101 CAGAGACTTT TAGTACTTTC ACTAATTTTG CTACTGTTAT CTAAAAGGCA 5151 GAGCCAGGTG TACAGGGTGG AACATGAAAG TGGACTAGGA GCGTGACCAC 5201 TGAAGCACAG CATCACAGGG AGATGGTTAG GCCTCCGGAT AACTGCGGGT 5251 GGGCCTGACT GATGTCAGGC CGTCCCACAA GAGGTGGAGG AGTAGAGTCT 5301 TCTCTAAACT CCCCGGGGA AAGGGAGATT CCCTTTCCCG GTATGCTAAG 5351 TAGCGGGTGT TTTTCCTTGA CACTGACGCT ACCGCTAGAC CACGGTTGGG 5401 TCCGCTTGGC AACGGGCCTC TTCCCAGATG CTGGCGTTAC CGCTAGACCA 5451 AGGAGCCCTC TAGTGGCCTT GTCCGGGCTT AACAGAAGGC TCTCACTCTT 5501 GTCTTCTGGT CACTTCTCAC TATGTCTCTT CAGCTCCTAT CTCTGTATGG 5551 CCTGGTTTTT CCTAGGTTAT GATTGTAGAG CGAGGATTAT TATAATATTG 5601 GAATAAGAG TAATTGCTAC AAACTAATGA TTAATGATAT TCATATATAA 5651 TCATATGTAT GATCTAGATC TAGTATAACT CTTGTTGTTT TATATATTTT 5701 ATTATACTGG AACAGCTCGT GCCCTCGGTC TCTTGCCTTG GCACCAAGGT 5751 GGCTTGCCAC CCACAGCCTC TCGAGTAGCT GGGATTACAG CCATGTGCCA 5801 CCATGCCTGG CTAATTTTTG TATTTTTGGT AGAGACAGGT TTTCACCTTG 5851 TTGGTCAGGC TGGTCTCGAA CTCCTGACCT CGTGATCCCC CACCCCCAC 5901 CCCCAGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCCA CTGCACCTGG 5951 CTGAGTTGGA GCTTTTCTTC CCTCTTTTTG GACTTTGGAA AATGCTCTTG 6001 GTCCATGATG CTATGTAGAC AGCTCCCGTT GACTGTGGCC TGTGCGGCAT 6051 TGGGCAGCAC TCTGGTGAAC ACTGAATCGG GTCTGACCTC CTAGCCCCAC 6101 CATTTACTGG CTGAGCCTCA GTTTCCTTGC CTGTAAAATC AGGAAGATGC 6151 TGGCTCTGCT CCTCTCTGCA CATTTCCCCG TCCTAACAAC ATTATAACTG 6201 TTAGGAAAGA GACGGGCTTG TTTTGGGATG GCTCATTTTA TGTGACCCTG 6251 TGCGCTGTCT CTGAGTCCAT CTGCCCTTCT TCCAGGGTGT AGGGACCAGC

6301 CCCACAGGGT CGGTGGGTCT CTCCCTGTGT GCGGCGATGA GAGAGTGTAG 6351 AAATAAAGAC ACAAGACAAA GAGATAAAAG ACAGCTGGGC CCGGGGGACC 6401 ACTGCCACCA ATGCATGGAG ACCAGTAGTG GCCCCGAATG TCTGGCTGTG 6451 CTGTTATTTA TTGGATACAA AGCAAAAGGG GCAGGGTAAA GAGTGTGAGT 6501 CATCTCCAGT GATAGGTAAG GTCACATGGG TCACGTGTCC ACTGGGACAG 6551 GGGGCCCTTC CCTGCCTGGC AGCCGAGGCA GAGAGAGGAG ACACAGAGAA 6601 AGAAAACTTA TGCCATTATT TCTGCATATC AGAGACTTTT AGTACTTTCA 6651 CTAATTGACT ACTGCTATCT AGAAGGCAGA GCCAGGTGTA CAGGATGGAA 6701 CATGAAGGCG GACTAGGAGC GTGACCACTG AAGCACAGCA TCACAGGGAG 6751 ACAGGCCTCC GGATAACTGC GGGCAGGTCT GACTAATGTG AGGCCCTCCA 6801 CAAGAGGTGG AGGAGCAGAG TCTTCTCTAA ATTCCCCCGG GGAAAGGGAG 6851 CCTCCCTTTC CCGGTCTGCT AAGTAGCGGG TGTTGTTCCT TGACACTTTT 6901 CGCTACCGCT AGACCACCGT CCGCTCGGCA ACGGGCGTCT TCCCAGACGC 6951 TGGCGTTACC ACTAGACCAA GGAGCCCTTT TGCTGGCCCC GTCCGGGCAT 7001 AACAGAAGGC TCGCACTCCT GTCTTCTGGT CACACCTCAC TATGTCCCCT 7051 CAGCTCCTAT CTCTGTATGG CCTGGTTTTT CCTAGGTTAT GATTGTAGAG 7101 CGAGGATTAT TATAATATTG GGATAAAGAG TAATTACTAC AAACTAATGA 7151 TTAATGATAT TCATATATCT CTAAGATCTA TATCTGGTAT AACTATTCTT 7201 GTTTTATATT TTATTATACT GGAACAGCTC GTGTCCTCGG TCTCTTGCCT 7251 TGGCGCCTGG GTGGCTTGCC GCCCACACAG GGCATGTCTG GATGGTTTGA 7301 ACACTAGGGC TTCTGATGCT CTAAGCCAGA GTCAGGTATT CATTCCATGG 7351 CACATGTGGC TGGGGTCTGC CCTGAGACCT GTCCCGTGCC AGGCTCTGGG 7401 GGCACATGGC TGATGGAACC AAGCATGGGG AGTGAAGGTG GAGGGTGGCC 7451 TGTGAGCACC ATGCCTGAGA GGACCAGGCT GGGGACGGAA GGTTCTTAGT 7501 GGATAATATT TATTGTCTCT GCCTCCCCC TGACATTTGC AAAGCGGCAT 7551 ATGCTTGTAA AAAAATTTTG AAACAGAAAA ATATAAATAA ATAAGTAGGT 7601 ATTACCACAT GCAAGGGTGA CCAATTTTGT ATTTTTCTTC CCAGCAGATG 7651 TTAAAGCAAG ACCAACAGTC TCCCCTCATG GAAGGCCCAC TGATCTAAAA 7701 TGCTGGTTCC TTTTGGACCT TCAGGGCACT TGGGGGAGAC CTTCCTGAGG 7751 TGCTGTGCAG TGTCTGGTGT TTCTCAGACC CAGGTGGTCA TGGGAGCCAG 7801 GCGTGGCTGA GTGGGCTCTA CAGGCCCTAG GCAGGGAGCA TCGCCTGTGC 7851 TGTGGCTGAC GTTCCTTCTG GCCCTGTTCC CAAAGTTCCC CATGGGGGCC 7901 TGGGAGGAAT GGCCTTTCCA GGGGGTGTTT TTATGAGAAG GAGGTAGCTC 7951 CCTGTTGGAG TGAGGTGCTC AGGAGGAAAG GGGCCTGGTC TTAGCAGTCA 8001 TGACCACCTG TCCCCAGTGA GGAACATCTC TCCTGCCACA CAGGCCTCCT 8051 GATCACTTGC CACGTGGCAC GCATCCCTCT GCCAGCCGGA TACAGAGAAG 8101 AGATTGTGCG GTACCTGCGG TCAGTGCAGC TCCCTGACGG TGGCTGGGGC 8151 CTGTGAGTGT GCCTGCCCCT GTGTCACTGC ACATGTGCAT GTGTGTGTTC 8201 TCATGATGTA GGAGATGCTT GGGTTTCCAG GCAGCTGCCA GGGGTTAGGA 8251 GTGATTGCAG CTGTGGGTGT GGGGTGGGTG AGGGAGAGAC TAGCAGGCGG 8301 GGAGTGGGCT GAAGGCCATG CAGGTGGGGC CTCGGCTTCA CATCTTTTGT 8351 TAAATGGATT TTGTGGCTGT TACGACACTC TTGAGACCCA CATGTGAAAA 8401 CTGTCAGTCT GTTATCACTT AAGACAGAAG AAAATTGCCC TTGACTCTGG 8451 GCTGGCAGCA GGTGGAGACA AGGCCTGACA GCTTTCCTGC CATGTGGCAC 8501 ACACTTTGGG AGCAGAGCCA TAGCCCAAAG TGGACCGCCC TTGAGCTAGA 8551 AGTGTTGACT CAGGCGTGGG AAGGTGTAGA GCAGGCGGGT CACGGTGAGG 8601 AAGGAGTGGG GGGCTCAGTT GTCATGGGAG GTGCATGAAT TCGTACTGCA 8651 GAGTGGCTGC TCAGGGGTCT CCTGTGTTGA CATGTTATGT CAGGTTAAGC 8701 CATTTTAGCA TTCTTAGTTT TCTGAGGAAA CTCCACAGAA AGTTTTGCTT 8751 TATTTCTTAG AAGTAAGGAC AGATACCGGT TTCTCACCTG TCCTCTGCTC 8801 CTGTAGGCAC ATTGAGGATA AGTCCACCGT GTTTGGGACT GCGCTCAACT 8851 ATGTGTCTCT CAGAATTCTG GGTGTTGGGC CTGACGATCC TGACCTGGTA 8901 CGAGCCCGGA ACATTCTTCA CAAGAAAGGT ACGGCATGTG CAGCATGTGC 8951 TGGGCCAGGG GTTCGTGTCA ACTCGATAAT GAGCTCTCAC AAACGAGATA 9001 CAGAAAGATG CACTTGCAGC TGAAACAGTG GGCAAAAGCA CATGAGCAGG 9051 GAATTTGTCA AAGCAGAAGT AGGCAGACAC TGTTTAACCT AGGCATCATT 9101 TTTTAAAAAA GCAAATTAAG AGCCAGGCAC AGTGAGTGGC TCACGCCTGC 9151 AATTCCAGCA CTTTGGGAGA CTGAGGTAGA AGGACCACTT CAACCTAAGA 9201 GTTCGAGGCC AGCCTGGGCA ACATAGTGAG ACCTGGTCTC TACAAAAACA 9251 ATAAAATATT AGCCAGGTGT GATGATATGC ACCTGTAGTC TCAGCTACTT 9301 GGAGGCTAGT AAGGCAGGAG GATCACTTGA GCCCAGGAGT TCTGGGTTGC 9351 AATGAGCTGG TTGTACTACT GCACTCTAGC CTGGGTGACA GAGTGCGACC 9401 CTGTCTCTAA TAAAATAAAA AAGCCAAGCA AACTAAGACA ACCAGGTAAT

9451 TCTGTTTGTT TCCTGAATTG GCAAAAACTT AAACGAACCG TGTTAATATG 9501 TCCACCTTCT GGGGGGCAGC CTGGCTGCAG GCAAGAGCAG CCCTGGAGCT 9551 TGCACCTTCC AAGCTGATCG TCTACCTCTC CAAGCCCGGG GCTGTCCACC 9601 TCTCCAAGCC CGGGGCTGTC CACCTCTCCA AGCCCGGGGC TGTCCACCTC 9651 TCCAAGCCCC GGGCTGTCCA CCTCTCCAAG CCCCGGGTTG TCTTACCTCT 9701 CCAAGCCCCA ACTGTCTACT TCTCCAAGCC CTGGTCTGGC TACCTCTCCA 9751 AGCCCTGGGC TGTCCACCTC TCCAAGCGCC AACTATCTTT CTCTCCAAGC 9801 CCTGGCCTGG CTACCTCTCC AAGCCCCAGG CTGTCCACCT CTCCAAGCCC 9851 CAACTGTCTA CCTCTCCAAG CCCCGGCCTG GCTACCTCTC CAAGCCCCTG 9901 GCTACCTCTC CATGCCCGGC CTGGCTACCT CTCCTCTTGC CTATAGGCCC 9951 TGAGGGGCAA TTCCAGCCCA AGGGAATCCA TGGCTCCTGC TGCTCCAAGA 10051 TGTGTTTCAC AGACCTTCCG TAGCCAGTCC CACCTGCCCT GCTCTCTGCT 10101 GCATGCGCAG GGGCCTCCTG TCAGCTCCTC AGAGACCCTT ATTATCCCAG 10151 GGCTCGCCAT GCACTGCCTC CTTCGCCTGG AGCCTCTTAC CTTCCACTCC 10201 TGCCCGCTG GCTCACACTT TACGTGTTCC TTCTTTGAGG ACCTCTTCCT 10251 GACCTACCGT GCCAGGTGGA GTGTCCTGTT ACGCATTCTC ATGAGATCCT 10301 GCCTTCTTTC TTGGTGAGCT TGTCACTATT GTCCTCAGTT CACTGTCAGC 10351 CTTTGGTGTC GTTGATGCTG CGTCCCCAAG GCTGCTGTCC GGTTCCCACC 10401 ACACTCCTGG CGCCTGCCTG GTGAAGGAAC GTGTTTAGGC TGCACTTTGC 10451 CTAGTAGCTT TGTGGGTCTT TATTGACTTT TGCATACCTT TTGGGGTTTG 10501 GAGCAGGAC TCCTCAGAAG CATGTTTAGA TGGTGTGGCT GTGCCAGGAC 10551 TGCTGCTGCT GAAGTGGCTC TGGCATGGGG CCAGCGTGCT GGAGCTACTC 10601 TGGAGTCTAG GGTCGTCTTT GTTCCCATAC AGGACCAGTC TGCCAAGTGG 10651 AGATGACACA GACTGGGGCA GCTCAGGCTT GGCTCAGAGG GCGAGGCTGA 10701 GTGTGCGCTG TCACTTCCCC ACCTTGCCTT CTCCAGGCGC ATGTGCACCT 10751 GGGCCCCTCG CTCACCTGAG CACTGAGGTG TCCCTGGACC TTCCCAGGTA 10801 GCTGTCTTCA TGTGCTCCTT CCTGGGGCCA GGGGTTGCAA ACACCTCTCC 10851 TGGGGCTGGA CACACACAC CCCAGGAAAG CCACTGGTTC CACCTAGGGG 10901 GCCGTGTATC CAGGCAAGTT CTCAGCACTC TGGAACCTGC TTCGCACATG 10951 GGGGTCGCAA GATCCACATG AGGCTGCCCT TGCCTCATGG AGAGGGGCAC 11001 ACGTGACTCC CAGAGGGTGA AGCTTCCCAG CTAGAGGCAG TGCAGACTTT 11051 GCTGACAGGA AGCAGATGAC GTGGGCCTAT TCTCTCCCCG CTCAGGTGGT 11101 GCTGTGGCCA TCCCCTCCTG GGGGAAGTTC TGGCTGGCTG TCCTGAATGT 11151 TTACAGCTGG GAAGGCCTCA ATACCCTGTT CCCAGAGATG TGGTATGTCT 11201 GCTGTTGATT GGGTTGTTGG GTCGCTGCTG CTGTCCCGGG GAGTAGAGTG 11251 ACAGGACCG TGGGTCAGGT GCAGGCTGTG ACAGCAGAGA GGGGTGGGCA 11301 TTCTGTGGGT GGGTGGAGTT AGGCTCCTGG CAGAGGCCCT GATCAAGCTT 11351 GAGTCCTGTA GGGGTACAGA AAGGGGGAGG TTCCCAATTG AGCAGGAAGA 11401 AGGCTGTGCC ATGGATGGAG GTACCCCGAG TCAGGCTGCA GGCAGGGCTG 11451 GGTGGCTTCC CTCTTGCTGT GGAAGACTCA GCATCTGTAG AAGTGGGGGG 11501 GTGCCCCTCC CCCAGCCTGC ACAGGGGCGT CCTGTGTTGC TGCTGCTGCG 11551 TTTGTCTCCT TTGCTGGTGA ATGTGAAGTG TGTCCCGACG TGACACCTCA 11601 CCTGTGGACT CAGCGTGTGT GCCTTTAAAA GATCAGTGTC TGTGGCCAGG 11651 TGGGGTGGCT CATGCCTGTA ATCCCAGCAC TTCGGGAGGC CGAGGCGGGC 11701 AGATCACGAG GTCAAGGGAT CGAGACCATC CTGGCCAACA TAGTGAAATC 11751 CCGTCTCTAC TAAAAATACA AAAATTAGCT GGGCGTGGCG GCGCGTGCCT 11801 CTAGTTTCCA GCTACTCGGG AGGCTGAGGC AGGAGAATCA CTTGACCCTG 11851 GGAGGCAGAG GTTACCGTGA GCCGAGATCG TGCCACCATA TTCCAGCCTG 11901 GCGACGGAGT GAGACTCTGT CTCAAAAAAA AAAAAAAAA GATCAGTGTT 11951 TGTTTTTTA AACAGAACCA CATACTGTTT AAATACCCAG CAAAATCAAC 12051 GAGTCTAGCT TTGTCACTCA GGCTGGAGTG CAGTGGCGTG ATTTGGGGTC 12101 ACTGCAACCT CCGCCTCCCG GATTCAAGCA ATTCTCCTGC CTCTGCCTCC 12151 CGAGTAGCTG GGATTACAGT CTCAGGCCAT CACGCCCAGC TAATTGTTGT 12201 ATTTTTAGTA GAGACAGGGT TTCACTATGT TGGCCAGGAT GGTCTCAAAC 12251 TCCTGACCTC AGGTGATCCG CCTGCCTTGG CCTCCCAAAA GTGCTGGGAG 12301 CCATGAGCCA CTGCTCCCGG CCTTATGTGG TGTCTTTAAC CAGTGTCTTG 12351 TAACATTTTA TGGCTATCTA TTGAAAGCAG TGGACATCTC CCCAGAAAAC 12401 ACTCGTGCAT ATGAGTTTAC CCCGTTATGC ATTTTGGGAA GTGAGACCCT 12451 GGAACCACA AGAGCCCCTG CTGGCTTCCT TGAGTGTTGT GGGAACCCTG 12501 GTGGGGGTGT CCCCTACAGA GCTATCATCA GGGCTGGGGG GGTCCCTTGT 12551 GTTAGATGAC TTTGGTGCGG GGGTGGGGGG TGGGGGGTCA AGTTAGGGGA

12601	GGCAGGAAGT	GAAGGGGCCG	CTCAACAAAC	CACACCACCA	CHCHCCHCM
12001	COLABORACI	CCCCCCCC	CICAAGAAAG	GACAGCAGCA	GTGTCCTGAT
	GCAAAGGCCG				
12701	GGCACAGGGA	TGGTGAGATC	ACCCCGGGAG	GGTAGACAGA	GATACCAGAG
	TAGGGGGCAG				
12801	AGGTTGGGAG	GTGTCCTGGG	GCCATTCAAA	TGCCCGCTGG	ACTCTGCGCC
12851	TCGCCCGTGT	GTAATGAGCG	GCAGAGGAAG	GACTGAGACG	GCAGTCAGCA
	CAGCTGCCAG				
	GGCGTCTCAT				
	GGGCACGCCA				
	TTGGGAGGTG				
	GCTGGAAGTG				
	GTGGGTGTGA				
13201	AGGCTCAGCA	TTGCTCACCC	TCACTTAAGG	ATGGGGCTAG	CATCACATAA
13251	GGCATCACAT	AAGGATGGGG	GCTAGCAGGG	AAAGGGAGAG	AAAACACATG
	AGGCACACAC				
	ACCAGTGATC				
	CTACAGTTTC				
	GAGTCTCTCG				
	ACTGCAACCT				
	GTAGCTGGGA				
	TTTAGTAGAG				
13651	TGACCTCAAG	TGATCCACCA	GCCTCGGCCT	CCCAAAGTGC	TAGGGTTACA
13701	GGCGTGAGCC	ACCGTGCCCC	TCCTAAAGTT	TCTTAAATAC	ACTTTTAAAA
13751	GTAAACTTTA	AATTTTGGAG	TAGTTTCCAA	TTTCTGGAAA	AGTTGCAAAG
13801	ATAGCCAAGA	GTGTTCCCTG	GGGCCCTCAC	ACCATATCCC	CATTGTTGAT
	GTTTTATGTT				
	TCCTAAGCAT				
	ACCGAACTAG				
	TGCCCCTCAG				
	GGGGAATAGC				
	ATGCTGGCGG				
	GCTGTTGCCC				
14201	CTCTGGTGCC	ACTGCCGGCA	GGTGTACCTG	CCCATGAGCT	ACTGCTACGC
14251	CGTTCGGCTG	AGTGCCGCGG	AAGACCCGCT	GGTCCAGAGC	CTCCGCCAGG
14301	TAGGACCTCA	TCAGGGAACA	AAGTGAAGGC	CTCTGGGGCT	GGGACCCACA
14351	GGGCCTGGGG	CTTCTGGAAT	CTAACCACAC	CTGTCCACTC	ACCTGGTGGC
	CCTGTGGAGC				
	TATAATAAAC				
	CAGTCAGTAG				
	GGGATGCAGG				
	CGAGGTTTGA				
	GGGGCAGAGG				
14701			TCCTCCCATA		
	GGGGTCAGTT				
14801	CCTGAGGGCG	GATGGTGGGA	GGCCACCCCT	CCTGGTTTGA	GCCAGGCCTA
14851	CCAGGTGCTC	CCAGGCCCCA	AGGCTCAGAC	ACTGCCCCTA	CCAGGAGCTC
14901	TATGTGGAGG	ACTTCGCCAG	CATTGACTGG	CTGGCGCAGA	GGAACAACGT
14951	GGCCCCCGAC	GAGCTGTACA	CGCCGCACAG	CTGGCTGCTC	CGCGTGGTAT
15001	ATGGTGAGCG	CCTCCTGAGG	GGCCGGCAGG	GCAGCCCAGG	GTCAGGGTCA
	GGGTGTCGCC				
	CACCTCCTCT				
	TCCACCCTGA				
	AAGGGTGTGT				
	GGAGCTCAGA				
	AAGGGCAAGT				
	GTCATGGTGT				
		0300300303	GTGCCCACCT	GCGGCAGCGG	GCCGTGCAGA
15/51					
TOADT	CCTGTATGAG AGCTGTATGA				GAGCATCAGC
	AGCTGTATGA	ACACATTGTG	GCCGACGACC	GATTCACCAA	
15501	AGCTGTATGA ATCGGCCCGG	ACACATTGTG TCAGTGCCCC	GCCGACGACC TGCCCGGCCT	GATTCACCAA CTGACTGCAG	CCCCTGGGGG
15501 15551	AGCTGTATGA ATCGGCCCGG TTGAGGTCCG	ACACATTGTG TCAGTGCCCC AAAGTGAAGT	GCCGACGACC TGCCCGGCCT CCTAGAGGCC	GATTCACCAA CTGACTGCAG GGGCTGTGAG	CCCCTGGGGG CTGGGAGTGG
15501 15551 15601	AGCTGTATGA ATCGGCCCGG TTGAGGTCCG GGTTTCCTGG	ACACATTGTG TCAGTGCCCC AAAGTGAAGT AGCCTGGTGT	GCCGACGACC TGCCCGGCCT CCTAGAGGCC ACCTCCATTT	GATTCACCAA CTGACTGCAG GGGCTGTGAG GGGAGGTGGC	CCCCTGGGGG CTGGGAGTGG CCTCTGATCG
15501 15551 15601 15651	AGCTGTATGA ATCGGCCCGG TTGAGGTCCG	ACACATTGTG TCAGTGCCCC AAAGTGAAGT AGCCTGGTGT TGAGGGCTTC	GCCGACGACC TGCCCGGCCT CCTAGAGGCC ACCTCCATTT TGTCCTGGAC	GATTCACCAA CTGACTGCAG GGGCTGTGAG GGGAGGTGGC CCCTGCACGC	CCCCTGGGGG CTGGGAGTGG CCTCTGATCG CCAGCTCAGT

15751 TGTCCTCAGT GTGCCTGGAC ACTCTCCTAG AGGCCCCTCC CTGAGATCTT 15801 GCTGGCTAGC TGGCTAGCTG GGAGGGGTGC TTTTTCCTCA CTTGGTTCCC 15851 TCTCCCCAAA CAGTTCATCA TTCGCCATTC TCCCGTGGGG TTTAGACATG 15901 CCCAGGGTGG GTGGGAGTAG CAGGTGCCAC TCCTGATTCC TCCTGCCTAG 15951 CTAGGGACTT GGAGCTCTCA CCTCTGTGGG GCCTGCAGGG GTCCAGGTGT 16001 GGCCAGTTCA GTGACCTTAG AGGGTGCAAT CCCCGGGCTG TGCTGGTGCG 16051 TGGCCGCCTC CTGACAGAGT CAGCAGGCCC TGGGCTGTGC TGCAGCTGCT 16101 GCCGTAGCTG TGCGCGTAGC TGCTGCGGTG TAGTGGGTTG GCTTAGGCAT 16151 TCTCTGGACA TACCCAGGTG GCACTGGGCC ACTGAGTCCC ACCCTGACAC 16201 TGCATCTCGG ATTTTCTGGG CCTCATGCCA CCTCAGTGGA TCACAAATCC 16251 TGACTGACCC TGCAGCGGT CCCTTGTTTT TTGCTCAGCA GTGATGTGGT 16301 TCTTTGTGGG TTTTGGTTTA ATCCCATATA GAGCACATCT GTACTAAACG 16351 CATTAGAAAC ATGCTTGCAA TTGGATCTTG ACTTGTGAGA TGCATAAGTA 16401 AAAAGTTGGG GGCCTCTGGA ACATTCTGTT CTGAGGAAGA AGGGGGGCAA 16451 GTGGTCCCTA CTGCTACAGT CCTGTCTTCG CATCTCTTCC TGGGCCCCTC 16501 AGGCCCTGTC CTCTGTCCCC TGTGTTGTCT CTAAGGCACC TGGTAGCCCA 16551 TGCCCCTCTG GTTTCTCCTG GAACCCCTCG CTTCTCCCTG GTGGAGTGCT 16601 GCTCCTTCTC ACAGCCTAAG GCAGGCTGTG GCCTTGGCCG ACACTGCCTC 16651 TGTCTGAGTT GGGTCCTGGG GACACAGTTG TTGCCCATCC TCGCTCAGGA 16701 AATGCCTGTT AGAGCAGAAG GCCCCTGTCC TGGCCCTGAG TGATCTGCAC 16751 GGCACTTTAT GCCTGGGGGC TGCTGTGGAT CTGGACGAGA CCTTGTCCCT 16801 GGAGGCTGCT GTGGGTCTGG AGCGGAGCCT TGACAGGGCT GTCTCTCCTG 16851 CAGATCTCGA AAACCATCAA CATGCTTGTG CGCTGGTATG TGGACGGGCC 16901 CGCCTCCACT GCCTTCCAGG AGCATGTCTC CAGAATCCCG GACTATCTCT 16951 GGTGAGTGTG GCTGGGATAT GCTGGCGGGG CCTCTCACGA AGACTGGATC 17001 TGAGCCCCAG CTGCATCCCA GTGAGGGGGC CCCCACGGTG CCATCTGGGA 17051 ATACTGCCAG GGAATACCTC CAGGAACCAG CAGTGTCAGG GCTTGTGGAA 17101 GCCACTGAGG GTTGTCTTTG AATTGGAAGA TTTGCCACCC AGTGGAAGTG 17151 TGGGGTGTTC CCAGAAGGTA GAGTGAGGAA GGGGGTGGTA GGTAGCAGGG 17201 CAGGTTCAGG TTGGCATCAG GAGGCCTGTG GACAAGGGGA GCTTGTCAGC 17251 CATGGACTGT GCCCTGGAGG TGGGGCCCCT GTCATGGAGG GCAGAGAGCC 17301 GTCCCATGGT GGGAAGCTTC CGCTGTACAG GCCTCTTCCT CTGGTGCCTC 17351 AGCACTGCAC GAGGGCGGCA GGGCTGGCAC AGCCTGGGGT CGGGGAGCCT 17401 CCCGCTGCCC CTTGCCTTGG GTGTGGCCCT TCTGGGTGAG TGTGTCCTGT 17451 TTTCCATAGA GTGTGGCCCT CACCCCCAGG AGCCCAGCAG CCCAGCTGGG 17501 GTGGCATCCA GGCCAGTGCC AGGCCTCGGG AGGGGACAGA CGGCCTCTCT 17551 GGGACCCTCC TGAGTGCAGG GTCTGGGTAG CAGCTGGGCT TCCAGCTTTC 17601 TCCTTGCACC TGACTTGGGC TTTTTTCTCC TCACAGGATG GGCCTTGACG 17651 GCATGAAAAT GCAGGTAAGG GCTGCGGGAC TGCGGCTGCA TGCTTCCTTT 17701 GCAATCATGT CTCCCCTTTA TTATTTTTCC TTTGGGGTTC AGAAATAACT 17751 CCTCCTGGAC CAGGTCCCGG CAGCGTGCGA CTAGAGGCTG AGTCAGTTGA 17801 GGCCTCTGGC CGTGTCCCTG TGGGTGCTGT TGGTCTCTGT GTGGGTGCCC 17851 ACCGTTCTCG ATGTCTGTCT GCAGCTGTCC TGTTTGCTTT TTGCCCTGAT 17901 GATCTGAGTG GGCTCAGCTG TGTAACGACA GACCCAGAGC TGCAGAAGCT 17951 CTCATCTTGT TACTGTGGCA GGAGGTGGCT CTGGTTAGTG GGGGCTTCTC 18001 CTCCATGCAC TCTTAATTTA AGGGGCTTCT TCTTAAAGGT CCTGGGTGGA 18051 CAGGACAGGA GCCTGGAGGA CCGTGGTGGC GTGTGGCCGG GCCTGGGAGC 18101 TCCCCGTGGA CTTGGCCTGA GTGGGCTGGA ACCCAGTCAT GAGGGGCACC 18151 AAGCACAAGG AGAGGGGAGG CCGGGTGGAT CCTGGCTGAC CCTGGTCCTG 18201 TCCTGGCTCT GGGGGCCCTG TAGACCGCAG TCCTGTCCGA CTGGGCTGAG 18251 CCTGCGCCCC TCTGTGCGTG TCAGAAGCCC AGACAGTGTT GCCCTGTGTC 18301 TTGTGGTCTA AGGAGGGTTA CGCCCTGCGG TGCCTGTCTT CTGTCCCCCA 18351 CCTGATTCAG TGTGGAAATG TGGAGTCTCC AGAGGTGTCC TGGGTGTCAC 18401 ATTTGGGATG GATACACGTG GGCCCAGCAC TGCCCGCCCC AGGGCTACCC 18451 TTGGTGCCAG GTGCCCCCAG CCACGAGCTT TTACCCAGCT GGCCTTGAGC 18501 TCCCCAGAGG CTCCCCGGAC ACTGTCCGTG TTTTGTGAAA AGGTTTTCAA 18551 AACACATGTA AAGTGGAGGT GAGTAGCAAG CCCTAGAGCA GGCCCTGGCC 18601 TCCCTGCCC TCCCTGTCCC CTCCCTGCCC CTCCCTGCCC AGCGCTCCCT 18651 CAGCACCGAC TCATCAGTGC ACCTCAAGCT GATGAGGGCG TCTGTGTTTT 18701 GACAAAATTG CTCTGAGGTT GTCACACCCA ACAAACTTAT GACGGTTCCT 18751 GAGTGTAGTC CTCACGTTGT GGCTGGTGTT TGTGAATCAG GATTCAGGCC 18801 AGGCCTGCAC AGGCCTTCAG TTGTTGGTCT TTGAGCTCCT GTTAGTCCAG 18851 CCGTCTCTG TGGTCTCTTT TCTCCTCCTG GAAGGTTTGT TCCTGAAGGG

18901 CTTCACATTG CAGATCTGAC TGGTTGCTTC TTATGTTCCC TGAGTTTTTG 18951 TAAACTGGCC AGGCCCTGAG GCTCGATCCC ATTGTGTTTC TTTGGCGAGA 19001 ATGCTTTTCT GGTGGTCCCT GCCTTGTCCC TCCAGTGCAC GATGTCTGGA 19051 TGCCTCTGCC ACACACCACC CCCTGCCCAG TCCCCATGTC TGTCTGGTCA 19101 GTGCCCAGCT CTGTCTCACT AGGGTTTGGT CACCGGCCCT TTGAACTGAG 19151 ACCAGGCTGT GTACCTGTGA GCCCAGCTCG GGGTGAGATT TGAGGTGGAG 19201 CCTTCCCAGC CCTGTGCAGA ATTCCCATCA CCTCCAGGTG TACTCAGAAA 19251 TGGGGATCAT TGGCCAGGTG CGGTGGCTCA CGCCTGTAAT CCCTACACTT 19301 TGGGAGGCCA AGGTGGGCGG ATCACAAGGT CAGGAGATAG AGACCATCCT 19351 GGCTAACACG GTGAAACCCC GATGCTACTA AAAAATACAA AAAAATTAG 19401 CTGGATGTGC TGGCAGGAGC CTGTAATCCC AGCTACTCCG GAGGCTGAGG 19451 CAGGAGAATG GCGTGAACCC AGGAGGCGGA GCTTGCAGCG AGCTGAGATC 19501 ACGCCACTGC ACTCCAGCCT GGGCAACAGA GCGAGACTTC ATCTCAAAAA 19551 AAAAAGAAAT GGGGTCATTT CCAGGCATCA CCATGACTGA GGTGCGCCAC 19601 TGTCATTGGG TGAGAGCAGC TGGATGCTCT ATGTGTAGGT GCTGGAGCCT 19651 CTGAGGGATC GTCCAGTCCT AGAAGTGTCC TCAGAGGGAC ACTGTCCTGC 19701 CTGGTGGCCC ATGAAGAAG GGAGGGCTCC CTGAGTCTCC CTGACGTGTG 19751 TCTGCCTGCA GGGCTCAGCC TTCTCTGAGG CCCTTGTCAG CCATGAGGGG 19801 TGCCCAGGGC TCAGAGCCTG AGGCTGAGCG TTGGCTGGGT GGGAGCCCCC 19851 ACACCTGGCC CTCAGGCGCC CATTGGATCC TGGAGGCAGT GGCTGGGAGT 19901 GGGAGGGGCT GCATCTGCTG CTGTAACACC ATCCTTTGTG TGTAGGGCAC 19951 CAACGCTCA CAGATCTGGG ACACCGCATT CGCCATCCAG GCTCTGCTTG 20001 AGGTTCGTGG CTCCTTCTCT TTTCTCAGCC TCAGCTGACC TTCCTGTGCA 20051 CGTAAGCCCA CGCATCCACC TGAGGGCAGC ACTGCTGGCC ACACACTTGC 20101 CACTCCTGA TACTTCCAGT GACCTGGGCT CTGGCCTCTG GCTTCAGAGG 20151 GTCGTGCTGT GGAGGGGGCG GCCTTGGCCA GCAGCCTTGG GTGTTGGGCT 20201 GGGTCGGGGG CCTTGGGAGG GCAGGGGCTG GAGGCTGTGT GAGAAGGGGA 20251 GTCTGGTGAA GGCTGTTTCT GAGAGTGCAG GCAGGAGTGG GACTCCAGGC 20301 TCTTCTTAGA ACTGGAACTG CTTGGGCCAG GCACGGTGGC TCACACCTGT 20351 AATCCCAGCA CTTTGGGAGG CCGAGGAGGG TGGATCACGA GGTCAGGAGT 20401 TCAAGACCAG CCTGGCCAAG ATGGTGAAAC CCCGTCTCTA CTAAAAGTAC 20451 ACAAAAATTA GCCAAGCGTG GTGGCGGGCA CCTGTAATCC CAGCTACTTG 20501 GGAGGCTGAG GCAGAGAATT GCTTGAACCC GGGAAGTGGA GGGTGCAGCG 20551 AGCCGAGATT GTGCCACTGC ACTCCAGCCT GGGTGACAGA GAGAGGCTCC 20601 GTCTCAAAAA AAAAAAAAA AAAAAAGAAC TGGAACTGTT TGTTATGGGC 20651 ATTCTCGAGC CAGTACTGGA GAAAAACGAG AGTGGATTTT TATGCCGGTG 20701 GGAATGAGGT AGGTGGGATT CTGAAGGTGT TTCTGGAGAG CCCTGAGGGC 20751 TGGGCCACGC AAAGGGCCTG CCTACACAGG GTGCTGGAGA CCCTCTGGGC 20801 ATGGATGCTG GCCAGGCAGG GGGGTGCTGG CATCCATAAA TGGTCTCCTG 20851 CGCCCTTCCA TCTTCAGTCA TATCTCATGG ACTTTTGCTG TTTTGTCTTT 20901 AAAGGTAAGT GCAGCAGGAG ACCCTGGCAC TCTCTGGAGA TGTCTGCTGG 20951 TTTGATTCTG GTCCCCGGTT GGGGCAGGAT GTGGCCAGGA CCATCGGGAA 21001 ACCAGCGCAG CCATGCTGGC CGTGCAAGGG CAGCTGAGCC TCTCTGTCCT 21051 GCTGTCTCTT CCAGGCGGC GGGCACCACA GGCCCGAGTT TTCGTCCTGC 21101 CTGCAGAAGG CTCATGAGTT CCTGAGGCTC TCACAGGTGA GGCCGGTGCC 21151 TGGGGCTCTG AGGGGGCTGA AGAGGGGGAT CAGGGCTGGG AGCTCCTGCA 21201 GGCAGAAGTG CCCACCTCAC CTCCACCCTG CCCTATTTCC TGCACTGGTG 21251 TTTCAGGGTC ACCCCCACCC TCCCATCCCC TCCCTAGCCC CTGCTCCATC 21301 CACCGGTCCT CCTCGGGCTG GCCTCACCTG GGGCAGTTCT CTGAGGCCTG 21351 CAGGGTGCTG GGGGTGCTGG CAGTTTCTGC GTCCTGCTCA TGTTGGAGCC 21401 ACTGTGTGCA AGGGCCAGGC ACGGGCAGGG GCTGTGTACC CTGAGCTGCA 21451 CAGCCTACAC GGCACCTCCA TGTCTCTGAA GCACCTTCTG CCCATGGAGG 21501 TGACGCCAGC CTGTGGACTT GCCCTCCTGA GACTGTTTGC AGCAAAAGCC 21551 CCGGTCCCTC CTGCCAGATC AGCTGCCCAC AGACCCTGCC CGAGCCCATA 21601 GTTTGACCTC AGTGTCTCTC ACACGTGCCT GCACCCCAGT CTGCAGCCAC 21651 AGTCATCCCA TACATGCGCC CCAACCTCCC GTGTCTCCCA CACCCTGTCC 21701 CGGCCACGGC CTCAGCCAGT GTCCCTCTGC CTGGAACCGC TGCCCCCAG 21751 CCCCGTCTCC CTCCCTTCAG CTCTCACTAG GACATTGTTC TGCAGGGCTT 21801 CTGGGTCTTC CTGGCCTCTG TGTGGCCAAG GCTGGCACCC ATCTTGGGCT 21851 CAAGCAGAGG AGGGGCATTG TCCTGCTGTG CCTGGCCCAA TGGCGGCCTG 21901 CTCCTGCTCC TGCCTCCTGC CCAGGACTTG CTCTGGGTGA TGGGGACTTG 21951 GGGAGGCTGA CTGAACCCTA CGGCACTCCA GGCCTCTTCC CTTCTCACTG 22001 AGGTGAGAGA GGCAGCCAGA AGCTGAGGTT GTTCAGGAGG CATTGGGGGC

22051	GCCTGGCACA	GAGCACACCC	GCAGAGACCT	GGGCCCCCTC	CCTGCCTTCT
22101	GGCCGGTGGG	GAGATCACAG	GGGAGTCAGG	TGCTGACTCC	CAGTCCCGTC
22151	TGGGCTGGTT	TGAGCCCTCG	CTGGCCAGTC	ACGTTTCCCA	GCAGCTGTGG
22201	GTGGTGAGCT	AAACAGGTGC	AGGCCCTCGC	GCGCCTCGCA	GCACCAGTGG
22251			AGCTCCCAGG		
	CTGCCCAGTC				
22351	GTGTTCTCTG	CTTCCACATT	TGCCCTCGAT	GCTGCCCAGG	TCCCAGATAA
22401	CCCTCCCGAC	TACCAGAAGT	ACTACCGCCA	GATGCGCAAG	GTATGCGGGA
22451	GCCAGCCCCA	TCCCTGTCCC	GTCCCCCAGG	GGAGGCCGCC	CTCAGCAGGG
	TGGGTCCTTC				
	GGCGTTTTTG				
	CTTCATGTTG				
22651	CACAGCCGTG	CCTCAGAGCA	GTTCCAGTGG	TCACGGCACA	CACAGGCTTC
22701	AGAAGGACAG	CCGAAGTGTA	GCCAGTGTGT	CCGGGGAAGG	CAGAGGAAAG
22751	AAGTAGACCT	CAGAGCCGGT	GTGGGCTGTG	ACCACAGGTG	CAGACTGTGA
22801	AATTAGGCAT	GGACCCAGCT	GCTGCTGCCT	GTTTACAATG	GGGGTGGGGG
	GCACCTGGGC				
	TGAGCTGCAC				
					-
	ATGTACCCAG				
	CCCTGCCCTG				
23051	GGGAGGTTCT	GAGAACTGGG	GTGTGGACAC	CCCCAGCCTG	GAGTCATGGC
23101	TTGTGCTCTG	CAGGGTGGCT	TCTCCTTCAG	TACGCTGGAC	TGCGGCTGGA
23151	TCGTTTCTGA	CTGCACGGCT	GAGGCCTTGA	AGGCTGTGCT	GCTCCTGCAG
	GAGAAGTGTC				
23251			TGTGGTCCCA		
	TGTCCTGCAG				
	CAGCACACAG				
23401	TATGTGGAGA	ACTGTGAGCT	CTGGCTGGAC	CCCTAGGGGC	CTTGCTGGGC
23451	TGTGTGCACA	GGGCCCTGCA	CTGCGGAGCT	GGTGTCCAGC	CCAGCCACCG
23501	ATACTTGGGG	GAGCCGGCGT	GGCCCCCAAG	GTTTCTCTCT	GGTGGTTTCC
23551	ACTGGGTGTC	TGAAGAGGGA	ATTTGTTGGT	GTTGGTTTTG	GTGCCACATC
	CTTTCAGCAC				
	TTTTCTGGCA				
	ATGTTCCCTG				
	GCTGCTTGGG				
	CCCCTGTTCC				
23851	TTCCGCTGTG	CCCTGGGCGC	CTGTGTGTGC	TCAGCACATG	GGCGAGTTCT
23901	AGGGTGCTCT	CTGTGATTTC	AGCTGCTGAA	CATGAGAAAT	CCAGATGGAG
23951	GGTTCGCCAC	CTATGAGACC	AAGCGTGGGG	GGCACTTGCT	GGAGCTGCTG
	AACCCCTCGG				
	ACCCGGGGCT				
	CCCCTTGCCC				
	AGCCCTCCCT				
	CAGGATCCTT				
24251	AGTGGAGGGT	TCCAGTGAGA	TCCACAGCCT	GGGCTGGTTC	CTGCTCAGTC
24301	CACAGGGCTT	GTGTTCTGTG	GAGGCTGCTG	TGTATCCAGA	GCGCCTGCAG
24351	GGAGGTGTCT	TTGGGGACTG	TGGGGACTGT	GGGGACCCAT	GCCATGGGCA
24401	GTAGGCTGCT	GTGTGTGCAT	GGTTGCCACC	GTACTGGTCT	TGGGGGAGGA
	TCTCAGCCCT				
	CCCTCCACAT				
	TGTTCCCCTC				
	GCCGGCGTTT				
24651	CTCACTGCAA	CACTCTTGCT	TGTTGTGGCT	TTGCCTGAGC	TGCAGAGCCT
24701	GGGCAGCCAG	GGTGAAACCC	AACACTTGGT	TCTTCCCTCC	CTTTCCCAGG
24751	GGACATCATG	ATTGACTACA	CCTATGTGGA	GTGCACCTCA	GCCGTGATGC
	AGGCGCTTAA				
	ATCCGGTAAG				
	GGCCAAGACC				
	CAGAAGCGAA				
	CCAGTCATAT				
	GCACAGTTAT				
	GAAGACATCA				
	TAACCTTTCC				

05001	omommommo.	200222020			
			AAGCGAACAG		
			CCGCCCCATG		
			TGCTCGCTTT		TAGGTGGACT
			TTGCCTTCTC		GCTCTCCTGC
			CGGGTAACAG		TCCCTCGGGC
			CCGCGCTATC		TTCTCAGCAC
25501	CTGGGAGGAT	TTCAGTCTGG	GTTATTATGA	AGCATCTACT	GTGAACACTC
25551	TTGTACTTAT	CTTTTGGGGG	CACCTGGGTA	CCCATTTCTC	ATGGTCACGT
25601	ACCTAGGAGT	GGCATTGCTG	TGTTAGAGGG	TACGTTATAG	GGTATGTGAT
25651			CCTATCACGA		
25701	TCAACCTGGT	GTAGACTCAC	CTTGGTCACA	ATGCACTGTC	CTTTTTATAT
			GAATATTTTG		
			ATAATTTTTT		
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			AAGAATTTAT		
			ATTACCGGAA		
			AAATTAGAAG		
			AGATGGGTTC		
			AATAGTTTAT		
			GTCTTCCCAT		
			TGTCCTCTTA		
26251	TGACATCCTC	CTCTTCCTTC	TGAGAATCTT	ATACTGATCT	TTTGAAAAAA
26301	AAAAAATCTT	AGTCTTTGAT	TCTGTTTTTA	AAGAGACTTT	ATTTTTGGTT
26351	TCATCAATTT	CTATTGTTTG	TTATTTTCTT	TCTTTCTTAA	TTTTTTTGAG
26401	ATGGAGTCTT	GCTCTGTTGC	TGAGGTTGGG	GAGCAGTGGC	GTGATCTCAG
26451	TTCACTGCAA	CCTCCGTTTC	CGGGGTTCAA	GCGATTCTCC	TGCCTCAGCC
26501	TCCCGAGTAG	CTGGGACTAC	AGGTGCTGAC	CACCATGACT	GGCCAATTTT
26551			AGGGTTTTAC		
26601			ATCCACCTTC		
			CACACTGGCC		
			CTTAGATATT		
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			GTGGTAGCAC		
	GTTTCTACTG		GCCCATGAGT		
			TCTGGTGTGG		
			CTTCACAGGT		
27001	TCCAGGGTCT		TGGCGTGGCC		TGCTGCTCTG
	CGGCATGAGG		TTGTCCTCAG		
27101	TTTTAAAAAAA	TAGATCATCT	TTTAAAAATC	ACTGTAATAA	AAGTAAAGCA
	GGTTCTTTGC		TGCAAAATAC		AAAGAAGAAG
27201	CTAAGTCGCC	CCTCCTCGCC	CCTGAAGGAG	AATCTGCTGT	TGCTGTTTGG
27251	TCTCCACATT	TCCATGGCGG	CTTGCTGCCC	CTTTCACGCC	TGGCCCACTT
27301	TGTGCCTGGT	GAGGTTTCTA	AAAGCCCCAC	CCTTGAGCGC	GCTCCTCCAG
27351	CACGAGCAGT	AATGGCACAG	GTGTTGTGTC	ATTTTACTCA	GTAGCCTCTG
27401	GGTTATTTTT	CAGTTTTCCT	TGTTGTTTTT	TAGCTTTTCC	CCATTTTAAC
27451	CTTAACTGGT	ATTTTCTTGT	TAAATATTTA	TTCATGACCA	TTATTATTCC
			GTCCACCTGC		
			CTGGCCTGGT		
			GCAAGAGTAC		
			AAGCACATGT		
			GCCCGCAGGG		
			TTGGTGACTT		
			AGGGTCTCAC		
			CACCACAGTC		
			CTGAGTAGCT		
			AAATGTTTTG		
			GCTCAAGCAA		
28051	CAAATGCTGG	GATTACAGAG	TGAGCCACCA	CACCCAGCCA	TTTTTAAAAT
			TTTCATTTTT		
28151	TATTATGTTA	${\tt CAGATATTTT}$	CCCCTCAATT	TCTTTGTTCT	TTTTATCTCT
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			TTTTATTTA		
			CCCAGGCTGG		
					5100

			CCCGGGTTCA		
28401	CTCCCAAGTA	GCTGGGACTA	CAGGCGCCCG	CCACTACGCC	CGGCTAATTT
28451			GGGGTTTCAC		
			CCGCCCGCCT		· -
28551	ATTACAGGCG	TGAGCCACCG	CGCCCGGCCT	ATATTAAGAT	TTTAAACTTG
28601	CCGGGCGCAG	TGGCTGACGC	CTGTAATCCC	AGCACTTTGG	GAGGCCGAGG
28651	ССССТССАТС	ACAAGGTCAG	GAGATCGAGA	ССУФССФССС	TAACACGGTG
28701			ACAAAAATTA		
			GGAGGCTGAG		
28801	CGGGAGGTGG	AGCTTGCAGT	GAGCCGAGAT	GGTGCCACTG	CACTCCAGCC
28851	TAGGCGAGAG	TGCAAGACAC	CGTCTCAAAA	ΑΑΑΑΑΑΑΑΑ	GATTTTAAAC
28901			ATACAGTTTG		
				•	•
28951			TATTTTACTA		
29001	TAAATTCACA	AATTTATAGA	AAAGTTACAA	AAATACTGAA	AAGTGCTCCT
29051	GTTTACTCTG	ACTAGAATTC	TTTAGTGGGT	GGCACCCTAC	CCTGAGGGCT
29101	TCATGACCTG	TCCTCCCACA	TGATCCAGGC	TCTACCCTCA	GGGCTTCATG
29151	Δ ССФСФССФС		CAGGCTCTAC		TCATGACCTG
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	CCACATGATC	CAGGCTCTAC	CCTCAGGGCT	TCATGACCTG	TCCTCCCACG
29301	TGATCCAGGC	TCTACCCTCA	GGGCTTCATG	ACCTGTCCTC	CCACGTGATC
29351	CAGGCTCTAC	CCTCAGGGCT	TCATGACCTG	TCCTCCCACG	TGATCCAGGC
29401	ТСТАСССТСА		ACCCTTCCTC		
	CCTGAGGACT	TCATGACCTG			
					TCTACCCTCA
	GGGCTTCATG				CCTCAGGGCT
29551	TCATTACCTG	TCTTCCCACA	TGATCCAGGC	CCATTCTTTC	TTGAACCATT
29601	GGAAAGGAAT	TTGCAGATAG	GATGTGTACC	CCTAACTGCC	TGAGTATTTC
29651	TTAGCAGGTG	ተልተተርተተተተናር	TGCAAGTGTA	ΔΩΤΌΔΩΔΔΤΩ	TTAATGTTGA
29701			CTAATTGTTC		CTTTATGGCA
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29851	GCACATGGGT	TGCATTTAGT	TATCACATTG	ACACCCTTTT	AACCTGGAAT
29901	ΑΑΨΨΟΟΨΨΑΑ	ጥርጥጥጥርርጥጥር	TGTTTGATGA	СФФФСФС Δ ФФ	TTTGAATTGT
29951			ATATCCTCAG		
					TTTCTGGTGT
			ATGAAACTAC		
30051	AGAAGAAATG	GGGCCTTCTC	CTGCACCTTA	CCAGGAAGCA	CACACCAACT
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30201			ATACCTGTTA		TTGATGATGA
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30301	TCCATATGTA	TTAGTTGGTG	TTCTTCCAAA	AGCTTTTCCT	TTGCCTCTGT
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			TTGCATTCAA		
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			CTATTTCACT		
			CTCAATAGCA		
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			AAGTTTTCAG		
			TATGGTAAGA		
			AGTGGCTGCA		
			TCCACATCCT		
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			CATTATGTTA		
			TCAGTGATGT		
			TTATTGTTGA		
			AGATATGTCT		
31451	GTGTCTTGTC	TTTTCATTCT	ATTAACAGTA	TCTTTTGCAG	AGCCAGTTTT

31501 CATTTCAAGG AAGTCCAGCT TATCAATGTT CTCTTTCATG TATCATGTTT 31551 TTGGTGTTGT ATCTAAAAAG TTACTGCCAA GCCCAAGGGT ACCTAGATTT 31601 TTTCCTGTGT TATATTCTAG GATTTTTAAA GTTTTGCATT TTACATCTAG 31651 GTCCATGATT CATTTTGAGT TAACTTTTGT GAAGGGTTTA TGGTTTGTGT 31701 CTAGATTTTT TTTTTTTTT TTTTTTTGCA TGTGGATGTC CAGTTGTTTT 31751 GGTACCATCT GTCAAGAAGA CTCTTTTTGG GTCATTTTGT TGCCTTTGTT 31801 TCTTTGTAAA AAATCAGTTG ACTGCATTTG CATGGGTCTA TTTCTGAGCT 31851 CTCTGTTCCA TTGCATTGAT CTGTTTGTTC TTCTCAGCAA TCCCACACTG 31901 TCTTGGTTCC TGTAGCTCTG TAGTAGGCCT TGCAGTCAGT TACCGCCCCT 31951 GTTCTCACTT CAGTGTTCTC TTCAATAGTG TTTTGACTAT TCTAGGTTTT 32001 TTCCCTCTC ATATACATTT TAGAGTCAGT TTGTCAATAG TTTACAAAAT 32051 AACTTGCTGA GACTTTGATT GGGATTACAT TGAATCTGTA GCTCAAGTTG 32101 GAAAGATCTT TTATTTCTTT CATCAGAATT TTGTAGTTTT CATCATATAT 32151 AGATCTTGTA CATATTTTGT TGTTTATACC TAAGGATTTC ATTTTTTTGG 32201 TGCTAATGTA AATGGCGTTG TGTTTTAAAT GTCAAAATCT AATTGTTCAT 32251 TGCTGGTAGG AAAACAACTG ACCCTTTTTT TTTTTTTTAA GGGACGCAGT 32301 CTTACTCTGT TGCCCAGGCA GAGTGCAGTG GTGCCATCAT AGCTCACTGC 32351 AGCCTCAAAC TCCTGGGCTT AAGGAATCCT CCTGTCTCAG CCTCCTGAGC 32401 AGCTAGGACC ACAGGCATGT GCCACTACGT TCAGCTAATT TTTCAATTTT 32451 TTTGTAGAGA TGGGATCTTG CTCTGTTGCC CAGGCTGGTC TCAAACTCCC 32501 GTCTGCTTTG AGATGATTAT ATATTTGTGT CCTTTGTTAA TTTAGAGGAT 32551 TATTATGGAT TTTTCTAATG TTAAGACACC TTTGTATTTC TGAGATCGAC 32601 CTTAGTATTG GTCTATATTT AAGACAGTAT TCAGTTTCTC AGTTGTTTTT 32651 TGTTTTTGG TTTTTTTTT TGAGACAGAG TCTCTGTCTC CCAGGCTGGA 32701 GTCCAGTGGC ACAATCTCAG CTCACCGCAA GCTCTGCCTC CCGGATTCAC 32751 GCCATTCTCC TGCCTCAGCC TCCCGAGTAG CTGGGACTAC AGGCGCCTGT 32801 CATCATGCCC AGCTAATTTT TTGTATTTTT AGTAGAGACG GGGTTTCACC 32851 ATGTTAGCCA GGGTGGTCTC AATCTCCTGA CCTCGTGATC TGCCCACCTC 32901 GATCTCCCAA AGTGCTGGGA TTACAAGGCG TGAGCCACTG CGCCCGGCAG 32951 CAGTTTCTCA GTTTTAATTT GGAGTTTTGC ATCTGTGTTC ATGAGTGAGC 33001 CTGAAATTTT CACTTTTCCA TATCTTATTT CTCTGGGTTC CTAGAATGAG 33051 CTAGAGAGTG TTCCTCCTTT CTGTTCTCTG GAAGAGTTTG TGTGAGATTA 33101 GAATGAGTGT GTCTGATAAT TTAGTTGCAT TCATTTATAA AATTCCTAGG 33151 CCTAGAGTTT TTTTTCTGGG AAAAGTTTAC ATTTTGACTC ATTTTTTAG 33201 TAGTTTTAGG ACTGTTTAGG TTCTCTATTT CTTGATTGAG CCAGTTTTGA 33251 TAAGTTAATC TTTCTAATTT GTAGATATTT TCTCTAAGTT TGCAAATGTA 33301 ATACATAAAA CTTTCTTGTC ATTTCTCACC ATATCTGTAG TTCTATCTTT 33351 TTATTGCTAA TATTACTAAT TTGTACTTTG ACTATTTGTA TTTGTTACCT 33401 GTTGCCGAGT AACAATATTA GTACAAACCT AGTGGCTTAG AACAACAC 33451 ATTGATTACT TCACCGTTTC TGTGTGTCAG AAGTCCAGGC GCGGCCTCGC 33501 AGGTCGTCCT CTGCCTCAGG GTCTCTCCGG GCTTCAGTCA GGGTGTTAGC 33551 CAGGACCGGG GTCTCGCCTG AGCTTCCAGT GAGGAAGGAT CTGCCTCTGA 33601 GCACACAGGG TCCTCGGCAC GATCCCATTC CTCAGCTGGA AGCTGCCGAC 33651 TGCCGTCTGC TGCGGGGCCT CTCTAGATGG CATCTTCACA AAAGCGAGAA 33701 GGGAGAGTTG GTAGAGGGAG TCTGCTAGCA CCATGGGAGT CGCGGTCACA 33751 CAGACCTCGG TCCCAGGACC CGCACCCATC AACCCTGCCG TGATCTGCTG 33801 GTTAAAGACA AGTCCCACGT CCCACAGGGT GACACTGGAG TAGACACTTC 33851 GCTCTGGCCT TTTCAGAGAA CTGGTTATTT TTTGGAAATA TCAGTTAGAT 33901 GTAGGATGGG TCTTGTCTTC TAAATCTATT GTTTTCTCTC TAATTGATTT 33951 TTTCCTGTTT TTATTTAGTT CACTTTGTTG GGTTTGCTCA AGCCTGGGTC 34001 ACTGGATCTC AGGGATGCTG CTCCTGTTTG CAGCTGTGTC TGCAGGGGCT 34051 TCCCAAGGCC TTGCTTTCCC CTCACGTCCC TTTCTCAGAC TCTGCCAATC 34101 CGCTTCCCGC TCTGGTGTCC TGTGGTTGCT TCTTTTTAAA ACCCTCATCG 34151 GTCTGTGTAA ACTGTTTATT TTTATGTGGT TTTTAAGGGA GACCATTCTC 34201 ATTCTTTTGA GACCCTGGAA AGGATGGAAT TGGGATAGGT AAACTGCTGT 34251 TTTACCAGAA TGTTCACTGG ACCAATCTCG TGTTCCAGGG AGACCCTCAC 34301 GCAGGGCTTA GAGTTCTGTC GGCGGCAGCA GAGGGCCGAT GGCTCCTGGG 34351 AAGGGTGAGT GAGCCTCCAC TCGTGAGTGC AGAGATGCAT GGGATCCAGA 34401 GGTTTCTGCT CTCACACACT GCGTTCATAA ATGTTGGCTT GTATGTTGTT 34451 GCTACACCAG AAGTTTCTGG AAGTGAGCTG CCAGCCCGTG ACTTCTGGGG 34501 GACCTCGTTC CTTTGTGGCA TGCGTGGCCT TTGCCCCGGT GGAAATTGCT 34551 CAGTACGTTG CTGGGCGCAG CCGGGCTGCT GGGAGCGCGC TGTAGCCTGA 34601 GCGTGGCTAT TCCCTCCACC CTTTCTGCTT GCTCTTAGGG TCCAGCAGAC

34651 AGAGCTGCTG TCTTCCACGG CCTTAATGCC TGAGGCACTG GAGTTGGTGG 34701 GCTGGCTGGG GCACGTGTGA TTGTTGCAGA ATGCGTGTTG TTTCACACAC 34751 CGGCTGTGAA CAGGGTGGAA GGGCTGAGGC TCTCCCTGTT TCCCTCCAGC 34801 TCCTGGGGAG TTTGCTTCAC CTACGGCACC TGGTTTGGCC TGGAGGCCTT 34851 CGCCTGTATG GGGCAGACCT ACCGAGATGG GTGAGTGAGT GCCTGTCCTC 34901 TGGTGGTGG GGGTTCTCAA CCCAATGCTC TGTCATGAGT GTTTTTTGCT 34951 TTGACATTTG GTTTTAGGGT TTGTTTGTTT GTTTGTTTGT TTTTGAGACG 35001 GAGTCTCGCT CTGTCAACCG GGCTGACATG CAGTGGCATG ATCCTAGCTC 35051 ACTGCAGTCT CAAACTCGTG GGCTCAAGCG ATCCTCCCGA GTAGCTGGGA 35101 TCACAGGTGC ACGCCACCAC CCCGGGCTAA TCTTTTAAAA CTTTTATGTA 35151 GAGATGGAGT CTTGCTGTGT TGCTCACACT GGTTTGGGCT CAAGCAGTCT 35201 TCCTACCTCG GCCTTCCAAA GTGCTGGGGT TACAGGCATG AGCCAATGTG 35251 CCTGGCCTGT TTTTAATATT TTTAAACAGT GAGATAAGAT CCCCGGTTGA 35301 AATGAAGATG TTTCCCTGGT CCCACAGCTC TCTGGAGCTT CCTGACATGT 35351 ATGCTGGAGG GACGCTTCTG GTCTCCGGCC CCTCCAGGCA TACAGATGCC 35401 TCCCAACCCT GAGTAGGAAG ATTAGGGTCC ACGGCCTCGC TGGAGCGGGT 35451 TAGAAGGCAG GAGATCTCCG GTCCCAGCCG TGTCTCCAGC CGCCGGACTC 35501 TCTCCCAGCC CTGTCTCCAG CTGCCCCACT GTCTCCCAGA GTCTGCCGTG 35551 TGGATGTTTA GAGGTGGGGA GCACCGTGCT TGGCTGAGTG CAGCTTGTGA 35601 GACGCTGCTC CCAAGCACTG CAGACCTCAC TCAGCCTGAC GCGTCCGTGA 35651 GGCCATCCTC GGTACTCGCA TGTCCCTTTG TCTTCCCAGC GACTCTGGGA 35701 GGCAGGAGTA TCTGTTCCCA GTTCACATCT GCAAAAGTCA AGCTCGGGTT 35751 TCAGTAGTGG CCCATGGCCC TTAGGTAGGG TGGCCCCATC GTGCAGGCTC 35801 CTCCCCGTAC CCCAAGGCAG CCTGCTGGGG TGAGAAGCCA GGGGTCTGGG 35851 ACCTTCCTTG GTGTGATGGT GTCTCCTGTC TCTGGTCTTT GCAGGACTGC 35901 CTGTGCAGAG GTCTCCCGGG CCTGTGACTT CCTGCTGTCC CGGCAGATGG 35951 CAGACGGAGG CTGGGGGGAG GACTTTGAGT CCTGCGAGGA GCGGCGTTAT 36001 TTGCAGAGTG CCCAGTCCCA GATCCATAAC ACATGCTGGG CCATGATGGG 36051 GCTGATGGCC GTTCGGTGGG GACGACGGGA CCGTCCCTGA GCCTTGGGTT 36101 TGGGTAGAGG AGGGACACTC AGCTGTGAGC CGGTGGCCTG GGCTGAGTGA 36151 ATGTAGAGAG GAGGGGAGGC CTGTGGGCCA GGTCAGCTGC CACTCTGGGA 36201 ACAGACACCT ACAAGAGCCA CATGCCTGGT TCCTGGGGCA AGAACGTGGG 36251 CTGCTCTGAC CAAGTGGGGC CCTGCAGAGA GGCTCGCCTC TTAGAAGTGA 36301 ACCACCCACC ATTAGCCATG TCAGTGGAAG AGCAAGCACA TCAGGGACCC 36351 ATGGAAACAG CGAGGTGGGC TGCGATGAGG ATGCTGCTTC CTGGTGTGGT 36401 AGTGATGACG GTCACAGCAG CTGCTCTCTG TGGCCCTACT GTGTTCACAG 36451 CTGGTGCTGA GCCACATATG TGCCAGGTGC ACACACACGC AGACGCATGC 36501 AGGCAGGCAT CAGTGTACAC ACTGATGTGC ACACACAGAT GTACATGGAG 36551 ACAGATGCAC ACACAGGCCT ATGCACACAC GTACGCATGC CCACACAGGC 36601 ACCTGTGTCC ACACACATAC AGATGCACCC ACAGCATCCC ATCTGTGCCA 36651 CACACTGACA TAGGTACATG GAGACAGATG CACACAGG TCTGTGCACA 36701 CACGTATGCA TGCACAGGCA CCTGTGTACA CACACGTACA GATGCACCCA 36751 CAGGATCCCA TCTGTGCCAC ACACAGACGT AGGTACATGG AGACAGATGC 36801 ACACACAGGT CTGTGCACAC ACATACATAC GCATGCACAG GCACCTGTGT 36851 ACACACATGC AGATACACCC ACAGCATCCC ATCTGTGCCA CACACAGACA 36901 TAGGTACATG GAGACAGATG CACACAGG TCTATGCACA CACATACGCA 36951 TGCACAGGCA CCTGTGTACA CACACGTACA GATGCACCCA CAGGATCCCA 37001 TCTGTGCCAC ACACAGACGT AGGTACATGG AGACAGATGC ACACAGGT 37051 CTGTGCACAC ACATACATAC GCATGCACAG GCACCTGTGT ACACACACGC 37101 AGATACACCC ACAGCATACC ATCTGTGACA CACACAGACG TAGGTACATG 37151 GAGACAGATG CACACACATG TCTGTGCACA CACATACATA CGCATGCACA 37201 GGCACGTGTG TACACACATG CAGATACACC CACAGCATGC CATCTGTGAC 37251 ACACACAGAC GTAGGTACAT GGAGACACAT GCACACAG GTCTGTGCAC 37301 ACACATACGC ATGCACAGGC ACCTATGTAC ACACATGCAG ATACACCCAC 37351 AGCATCCCAT CTGTGCCACA CACAGACATA GGTACATGAA GACAGATGCA 37401 CACACAGGTC TATGCACACA CGTATGCATG CACAGGCACC TGTGTACACA 37451 CATGCAGATG CACCCACAGT ATCCCATCTG TGCCACACAC AGACATACGT 37501 ACATGGAGAC AGATGCACAT ACAGGTCTAT GCACACATGT ACACATGCAC 37551 AGGCACCTGT GTACACACAT GCAGATGCAC CCGCAGTATC CCATCTGTGC 37601 CATACACAGA CATACGTACA TGGAGACAGA TGCACATACA GGTCTATGCA 37651 CACATGTACA CATGCACAGG CACCTGTGCA CACATATGCA GATGCACCCG 37701 CAGTATCCCA TCTGTGCCAC ACACAGACAT ACGTACATGG AGACAGATGT 37751 ACACACAGGT CTATGCACAC ATGTACACAT GCACAGGCAC CTGTGTACAC

37801	ACATGCAGAT	GCACCCGCAG	TATCCCATCT	GTGCCACACA	CAGACATACG
37851	TACATGGAGA	CAGATGCACA	CACAGGTCTA	TGCACACATG	TACACATGCA
	CAGGCACCTG				
	CCACACAGAC				
38001	ACATGTACAC	ATGCACAGGC	ACCTGTGCAC	ACATACATAC	AGATGCACCC
38051	GCAACATCCC	GTCTGTGCTG	CCCTATTAGG	TTTGTGGCCA	TTTGGGGAAT
	CTTCCTAAAA				
	GGGTCTGGGG				
38201	TGGGCCCGCT	GAGCCCTGGA	TCCTTCTTGG	TGTCTTATCC	TGGCCAGCAA
38251	GCAAGTGTGA	GCTCCTGTGG	GTCTCCAGAG	GCCCATGAGG	ACCAGTGGGC
38301	CAGTTGGGAA	CAAGGCTTGG	ССФССФСФФС	AGGGGGGAAC	ACCAGGGCAG
	GCCTGAGGAG				
	CAGGGAGCCT		TGTGGCAAGA		
38451	CTGGCGGGGC	CTGTGGGCGT	CAGTTTAGAC	CCATCCATTC	TCACTGCAGC
38501	ATTCCAGGGT	TTGCCCTTAT	GCTCGGCTGT	GTGAGGGTGA	GGATGATGCT
38551	GTGGGGGCAT	GCATGCTGGG	TGTGTTTCAG	CCTTCTCTTC	CACCAGGCAT
38601	CCTGACATCG	AGGCCCAGGA	GAGAGGAGTC	СССТСТСТАС	ТТСАСАААСА
	GCTCCCCAAT				
	CAAGGCCCAG				
38751	GCTCTGTGTC	CTTTTTGGGG	TACTTTGGAC	ACTTGGGAGG	CGTCACCTCT
38801	GCCAGTGAAT	GCCACAGTTG	GTGGCAGGTC	TGTGGCAGGT	GGTCGGGTCC
38851	TAAAGTCCAG	ATCTTGCTGT	TGTTTCAAGT	GATGCTCTGG	GTGGGGGAGG
	AGCTGGATGG				
38951					
			CTAGTGGCCC		
39001			GTCATGTGAG		
39051	ATGAGGCTGA	GTTGGTGGAA	GCTGATGTGG	TTGTGAGGGG	CTGGTGACCC
39101	TGGCTTAGGG	TTTGCTGCAG	GGCGGGGAGT	CTGAGCTGGG	CTGATGGTGC
39151	CATGACTGAT				
	AGCCCTTTCC				
	GCTCCAGTTC				
39301			GAAAACATTG		
39351	TGTGCCATCT	CCTACACGAG	CTACAGGAAC	ATCTTCCCCA	TCTGGGCCCT
39401	CGGCCGCTTC	TCCCAGCTGT	ACCCTGAGAG	AGCCCTTGCT	GGCCACCCCT
	GAGAACATGC				
	GGGGTCCTGG				
	AACCCCTCAA				
39601	GCAGGGATGG	GGACAGGGTG	GGTGGCTTAG	ACTCTTGATT	TTTACTGTAG
39651	GTTCATTTCT	GAAAGTAGCT	TGTCGGGCTT	GGGTGAGGAA	GGGGGCACAG
39701	GAGCCGTGAC	CCCTGAGGAG	GCACAGCGCC	TTCTGCCACC	TCTGGGCACG
39751			GGAGGTTTTT		
39801					
			CCTGTGTGAT		
39851			GGCAGGCTTC		
39901	GGGCTGAGGG	ACACGAGGGC	AACCCTGTGA	CAATGGCAGG	TAGTGTGCAT
39951	CCGTGAATAG	CCCAGTGCGG	GGGTTGCTCA	TGGAGCATCC	TGAGGCCGTG
40001	CAGCAGGGAG	CCCCATGCCC	CTGGGTCGTG	AGCTTGCCTG	CGTATGGGGT
	GGTGTCATGG				
	GTGGTGTCAT				
	CAGGGTCTGT				
	CCCCTGGGAC				
40251	CAGGGTTTAT	AGTAGTCTTG	TGGACACAGA	AATGCACAGG	GGACACTTAC
40301	GGACACAGAA	ATGCACAGGG	GAGGCCGAGC	ATAACCAGGG	GTGAGGGGCA
	GGCAGCAGTT				
	CAGCGCCCAG				
	CTGGGAGCCC				
	ATGCCCAGGT				
40551	GGCTTCCCCA	GGCAATCCTG	TGAGCTCCCT	TCTAGCCTCT	GACCCAGTCT
	GGTCTGGCTT				
	CTTTGCCTTT				
	GAGACTGTCA				
	CGTTACCCCT	GCTGCCTTGC			
40801					
	TCTTCCCCTC				
40851	TCTTCCCCTC	TCACTCTCCC	TCAGGCAGTG	GAGATCTGCG	TCTGGACACC

```
40951 CTTGGTGTGC GGTCCAGGGC TCTCACCCAG GTGCCGCACC CTCTGGGGTC
41001 TTCTGTCCAG CTCCCTTGCC CCATGTGCTG TCACTGACTC TCCTTGGGAC
41051 TCGCCTGCCT GCTCAGAGCC CTGCAGGGCT TGGTCAGCTG CCTGTTCAGT
41101 GTCAACACTT CCCTGCACAT CTTAAAACTG GGCTTTATTT TCGCTGAAGG
41151 AACTGTGTTG GGACCCTTGA CATCTGTCAG GTTTGCACAT GCTGTTTTTT
41201 TTTCTCAGCC CACGTGTTCT CCCCCACGTG GGGTAGCAGC AGGACAGACA
41251 GTGAATCACA GAGTCTGCCC TGAGCAGAGG CTGCTGTCCC TGGGACTCCT
41301 AGCCATGGTC AGACTGTACA AAACGGTTTT CCAGAAATGA AATGTAAATC
41351 CATTTTATA CTGAAAATGT TACTGAAAGT CACTTTTATG AGCATCTGCC
41401 TTAATAAACA GACATTGATT CCCTTATCAG AAGCCTGTCA CACTGTGTTT
41451 CGTTTCATCC TGGGGAGAAC TGCAGATTTG GGGTTTCTGG CTGTCATACG
41501 TCACCTGCCT GTGGGGCGAG TGGGAGGCCC AGCCTGGTTT AGGGAACAAG
41551 AGTGACGTGA GGAGTAGCAG GGTGCGTCTC CAGTTACCTG AGGGAAAACA
41601 GATATTTTAA GAGATAATAG CATAGCCTAT TTTAATATGT TTTAAAGGCC
41651 ATAAGCATAT CCAGGAAGAT AAATAAACGT GATACAATGT CCACATAGGA
41701 GGAACTTTCT TTCACTGCAT TGTTTTCCTT CACAGTGGCC TTCAAGTCAC
41751 AGGACGCAGC GATTCCCTGC CCTCTTCGGT GTTATTACAC AGGCAGGACT
41801 TCAGTGTCAG TATCCCTGCC TTCAGTCTTC TTTAGAAATC ACATCTGTGT
41851 TCAATCCATT GTTTAGAGGG AGTGTATTTT TCCTGTTCCA CGAAGAGGAC
41901 TTTTTGTTCA CAATTGGATC ACAATGCAGA GGAGTCTGTT CCTCCCCCGT
41951 CGGCTTCTCG GTGCTGGGAG GGTGACCTGT CCCAGATGAC TCATCACCCT
42001 GACATGCTCT TGACAAAGGA CACCACCAAG AGGAGATGGC AGCTGTACCG.
42051 GTGCAGCCTC TGTCTGAGGG GGATATTTGC CTCAGTGTGA TTAAAAATCA
42101 GTCATGAAAG ATTTTTGAAT TCAGATTATT TTTATCAGGA ACAGATTTTG
42151 AACATCCTGA AATCTTTTCC CTGGCATCAT ATTAGGTTTT CTTTGTTCAC
42201 TATGATGTAA AGTTTCAGAC TCTTGATATT TTTAATATCA ACATAGACGG
42251 TAGGACAAGG AACGGTACCA GAAATGAGTA AAGAGACAAT AATGATAAGA
42301 TCGATTTATC AAGACATAAC AACCCCAAAT GTATATGCAC TAAATAACAG
42351 CTTCAAAATA CATGAAGCAA AATGGCAGAA TTGAAGAGAA TGAGATAAAA
42401 ACAGAATTTT AACGGGTGCT TTCCGTACTT TGTAACTGAC AGACATGAGA
                                                              (SEQ ID NO:3)
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FEATURES:

Start: 2034 Exon: 2034-2047 Intron: 2048-2179 Exon: 2180-2345 Intron: 2346-3088 Exon: 3089-3227 Intron: 3228-8043 Exon: 8044-8119 Intron: 8120-8806 8807-8928 Exon: Intron: 8929-11095 Exon: 11096-11192 Intron: 11193-14163 14164-14299 Intron: 14300-14894 14895-15003 Exon: Intron: 15004-15390 Exon: 15391-15509 Intron: 15510-16853 16854-16951 Exon: Intron: 16952-17636 Exon: 17637-17664 Intron: 17665-19945 Exon: 19946-20002 Intron: 20003-21064 21065-21136 Intron: 21137-22389 Exon: 22390-22440 Intron: 22441-23113 23114-23263 Exon: Intron: 23264-23922 Exon: 23923-24019 Intron: 24020-24749 Exon: 24750-24855 Intron: 24856-34288 Exon: 34289-34354 Intron: 34355-34799 Exon: 34800-34880 Intron: 34881-35894 35895-36065 Exon: Intron: 36066-38596 Exon: 38597-38675 Intron: 38676-39320 39321-39449 Exon:

Stop: 39450

CHROMOSOME MAP POSITION:

Chromosome # 21

ALLELIC VARIANTS (SNPs):

THE THE	TH/TIME (P			*		
DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
478	-	A	Beyond ORF(5')			
891	С	G	Beyond ORF(5')			
948	-	C	Beyond ORF(5')		•	•
3311	A	${f T}$	Intron	- *	•	
3616	T	С	Intron			
3910	G	Α	Intron			
6028	G	A	Intron			
8299	G	Α	Intron			
8373	С	G	Intron			
8424	A	G	Intron			
8680	A	G	Intron			
8700	С	G	Intron			
8996	A	С	Intron			
10590	T	C	Intron			
11090	G	С	Intron			
11710	G	A	Intron			
12591	G	Α	Intron			
13431	-	T	Intron			
14746	С	G	Intron			
14975	G	С	Exon	277	P	P
16031	С	${f T}$	Intron			
16891	-	${f T}$	Exon	339		V
19359	С	T	Intron			
19405	A	G	Intron			
19653	G	A	Intron			
19742	${f T}$	С	Intron			
20054	A	G	Intron			
20627	_	A G	Intron			
21337	T	С	Intron			
21894	С	${f T}$	Intron			
23360	G	${f T}$	Intron			
26758	A	С	Intron			
27033	T	С	Intron			
27332	С	A	Intron			
27538	С	A	Intron			
27625	G	С	Intron			
27736	A	G	Intron			
30688	T	C	Intron			
31172	С	T	Intron			
31433	С	T	Intron			

FIGURE 30

32660	G	T	Intron			
32981	Α	С	Intron			
33557	T	С	Intron			
33652	G	Α	Intron			
34390	T	С	Intron			
34399	G	С	Intron			
34989	G	-	Intron			
35067	С	G	Intron			
35495	G	Α	Intron			
36001	T	G	Exon	631	L	v
38948	C	T	Intron			
39160	T	С	Intron			
40405	G	Α	Beyond ORF(3')			
40794	С	T	Beyond ORF(3')			
40961	A	G	Beyond ORF(3')			
41891	С	T	Beyond ORF(3')			

Context:

DNA Position

478

AGGTTCAGTGTGAGATTCCATCCAGGCTGAAGCCCCTTATCCCTATTCTTCATGTTTCTA
CATGGAGGAACTTACCTGGAGAAAAACTTCCAGCCTCTTTCTGCTTCCAGAGAAGTAGAG
TGACTCATTTGATTGAATTTCAGAGAACAGATAGGGTGGAGTGTGCTCAGGCTCCTCTGG
GTACTCTTTCTGGGGTCTGTGGGTTGACTGGAGGGGTGTCTTCTGGTGGGCACTCAATTG
CATAGTGCTTGGTGAGGCAGTTTCATGGCCTAGAGGCTGGGGGATATGTTTGTCTGACTT
[-, A]

891 TGTCTTTTCATCCGTTTCTGAACTGGGATAGGAAGAGTGATTATCCTTGATTGTCTAA
AACCCCGCTATTCCACTGTGGGGAAGGTGCCTGTGGGTATTCTTTTTGTCCACTCTCTT
CCAACTTTCTCCTCCGGCTTGCTGTGGCTCACCGCCCCTTCGAAGTTAGGCTGGGGTAG
GAATTGAGGAGTGGGTGCCGAAATGCTCACTAGGCTGGGGCAGTTGTAACTGGATGTCAG
GGCTTCTGTGGGCCAGGTGAAGACATGCTGGGGTCTTCTGTGGGTCCTTGACCTGACTTA
[C.G]

GGACCACTGGCTGCAGCCTCCAGACGTCAGCCATGTTTCCAACAGTCAGACGCCCCCTGC CCTGTTGCGCCCGGCTGTCCCTTCCAAGTTCGGTCACTCGCCTCCATCTTCCTCT TCCCTCTGCTGCTAAGGCTTTTCACCTTTAATTTCTCCTGGGGCCACCCCCAACTCCAGC GACCCCGTGAGCAGCTGAGGCTCTACCGCGCTCGGTCCTGGCCAGCGACGCAGCCCTTCC CTGGCGGGGCTCCAGGGCTTCTGGCCCCTGTGGTCCGCCAGGTGTGGGGGCCCACGGCCT

948 TAAAACCCCGCTATTCCACTGTGGGGAAGGTGCCTGTGGGTATTCTTTTGTCCACTCTCT
CTTCCAACTTTCTCCTCCGGCTTGCTGTGGCTCACCGCCCCTTCGAAGTTAGGCTGGGGG
TAGGAATTGAGGAGTGCCGAAATGCTCACTAGGCTGGGGCAGTTGTAACTGGATGT
CAGGGCTTCTGTGGGCCAGGTGAAGACATGCTGGGGTCTTCTGTGGGTCCTTGACCTGAC
TTAGGGACCACTGGCTGCAGCCTCCAGACGTCAGCCATGTTTCCAACAGTCAGACGCCCC
[-,C]

TGCCCTGTTGCGCCCGGCTGTCCCTTCCAAGTTCGGTCACTCGCTCTGCCTCCATCTTCC
TCTTCCCTCTGCTGCTAAGGCTTTTCACCTTTAATTTCTCCTGGGGCCACCCCCAACTCC
AGCGACCCCGTGAGCAGCTGAGGCTCTACCGCGCTCGGTCCTGGCCAGCGACGCAGCCCT
TCCCTGGCGGGGCTCCAGGGCTTCTGGCCCCTGTGGTCCGCCAGGTGTGGGGGCCCACGG
CCTCACCGCGCCTACCCCACTCCCCCGGCGAAGCTACGCGGCGCTCAGCTTCCCAGGGA

TGAAGCAGGTGAAAATCCAGGGGCTCACAAGAAAAGGGCTGGCAAACTCTGCCCTATGTC AGAGTCGTCCTGCTATTGGTCTAGGGGATCAGCTTAGCCTTGCCAGTGTAGGGTGACAGGC GGTGGGCTTTGAAGTCTCAGTACAGGATGGGATGGACATTCCAGGTGGAAGGCCCAGCCT

3616 GCAGGTGAAAATCCAGGGGCTCACAAGAAAAGGGCTGGCAAACTCTGCCCTATGTCAGAG TCGTCTGCTATTGGTCTAGGGGATCAGCTAGCCTTGCCAGTGTAGGGTGACAGGCTCTC GGCTTTGAAGTCTCAGTACAGGATGGGATGGACATTCCAGGTGGAAGGCCCAGCCTATGC CAAGGGGCTGTAGGTGGCAGAGTGGTGGGTGGGGAGCTGATATCTGCTGTGAACTTCCT

> GGGGCTATTGCAGGAGAGCTTCAGGTTCAGGCTGGTGAGTAGGAGGAGCATAGCAGTTGG ACTGCCTGGGTATTGAACTGATTTGGCTACACAAGACTATTTTGCATCCTGGGAGTGTTT CTCTACAGAAATCCTCAGCCTTGTAAAATGGGAAATTCCCTCCTATGAATTTATGCAATA GGACTTTTTTCCCTAGTGACTTGTAATCACATTGTTTCAATGACGTGAATTCCTACATAA

CTTCCTCGGGGCTATTGCAGGAGAGCTTCAGGTTCAGGCTGGTGAGTAGGAGGAGCATAG CAGTTGGACTGCCTGGGTATTGAACTGATTTGGCTACACAAGACTATTTTGCATCCTGGG AGTGTTTCTCTACAGAAATCCTCAGCCTTGTAAAATGGGAAATTCCCTCCTATGAATTTA TGCAATAGGACTTTTTTCCCTAGTGACTTGTAATCACATTGTTTCAATGACGTGAATTCC TACATAAATAGGTTTTGTTTCTGTGATAACTCTTACTGATACATCATTTTCTTTTACTAC [G, A]

> CTCTTACCTGTGTCTATTCATTTACTCATCCAAATTGCCTTTATCCTGATTTTGTCCCAG ACTTGAAATGAAGTTGCAATAGGCTTATATGTTAGTTTGGGAAGAGTTGGCCTTTAACGT TAAAAACAGTTCCATGGTGTTTACTGTAGGCCCAGCCCTGCTCAAGGCCTGTTCTTCTTT TAGTCCTTAGAATAAGCCTAATGAGATACATTAGAAAGCTGAGGCACATTTATTCCAGGT

6028 GTCTCTTGCCTTGGCACCAAGGTGGCTTGCCACCCACAGCCTCTCGAGTAGCTGGGATTA CAGCCATGTGCCACCATGCCTGGCTAATTTTTGTATTTTTGGTAGAGACAGGTTTTCACC TTGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCGTGATCCCCCACCCCCACCCCAGC CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCTGGCTGAGTTGGAGCTTTTC TTCCCTCTTTTTGGACTTTGGAAAATGCTCTTGGTCCATGATGCTATGTAGACAGCTCCC

> ${\tt TTGACTGTGGCCTGTGCGGCATTGGGCAGCACTCTGGTGAACACTGAATCGGGTCTGACC}$ ${\tt TCCTAGCCCCACCATTTACTGGCTGAGCCTCAGTTTCCTTGCCTGTAAAATCAGGAAGAT}$ GCTGGCTCTGCTCTCTGCACATTTCCCCGTCCTAACAACATTATAACTGTTAGGAAA GAGACGGCTTGTTTTGGGATGCTCATTTTATGTGACCCTGTGCGCTGTCTCTGAGTCC ATCTGCCCTTCTTCCAGGGTGTAGGGACCAGCCCCACAGGGTCGGTGGGTCTCTCCCTGT

8299 CATGACCACCTGTCCCCAGTGAGGAACATCTCTCCTGCCACACAGGCCTCCTGATCACTT GCCACGTGGCACGCATCCCTCTGCCAGCCGGATACAGAGAAGAGATTGTGCGGTACCTGC GCACATGTGCATGTGTGTTCTCATGATGTAGGAGATGCTTGGGTTTCCAGGCAGCTGC CAGGGGTTAGGAGTGATTGCAGCTGTGGGTGTGGGTGAGGGAGAGACTAGCAGGC [G, A]

> GGGAGTGGGCTGAAGGCCATGCAGGTGGGGCCTCGGCTTCACATCTTTTGTTAAATGGAT ${\tt TTTGTGGCTGTTACGACACTCTTGAGACCCACATGTGAAAACTGTCAGTCTGTTATCACT}$ TAAGACAGAAGAAAATTGCCCTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGAC AGCTTTCCTGCCATGTGGCACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCC CTTGAGCTAGAAGTGTTGACTCAGGCGTGGGAAGGTGTAGAGCAGGCGGGTCACGGTGAG

8373 ATCCCTCTGCCAGCCGGATACAGAGAGAGATTGTGCGGTACCTGCGGTCAGTGCAGCTC CCTGACGGTGGCTGTGAGTGTGCCTGCCCTGTGTCACTGCACATGTGCATGT GTGTGTTCTCATGATGTAGGAGATGCTTGGGTTTCCAGGCAGCTGCCAGGGGTTAGGAGT GATTGCAGCTGTGGGTGTGGGTGAGGGAGAGACTAGCAGGCGGGGAGTGGGCTGA AGGCCATGCAGGTGGGGCCTCGGCTTCACATCTTTTGTTAAATGGATTTTGTGGCTGTTA

> GACACTCTTGAGACCCACATGTGAAAACTGTCAGTCTGTTATCACTTAAGACAGAAGAAA ATTGCCCTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGACAGCTTTCCTGCCAT GTGGCACACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCCCTTGAGCTAGAAGT

> > FIGURE 3Q

 ${\tt CTCAGTTGTCATGGGAGGTGCATGAATTCGTACTGCAGAGTGGCTGCTCAGGGGTCTCCT}$

8424 TGTGCATGTGTGTTCTCATGATGTAGGAGATGCTTGGGTTTCCAGGCAGCTGCCAGGG GTTAGGAGTGATTGCAGCTGTGGGTGTGGGTGAGGGAGAGACTAGCAGGCGGGGA GTGGGCTGAAGGCCATGCAGGTGGGGCCTCGGCTTCACATCTTTTGTTAAATGGATTTTG TGGCTGTTACGACACTCTTGAGACCCACATGTGAAAACTGTCAGTCTGTTATCACTTAAG

> CAGAAGAAATTGCCCTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGACAGCTT TCCTGCCATGTGGCACACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCCCTTGA GCTAGAAGTGTTGACTCAGGCGTGGGAAGGTGTAGAGCAGGCGGGTCACGGTGAGGAAGG AGTGGGGGGCTCAGTTGTCATGGGAGGTGCATGAATTCGTACTGCAGAGTGGCTGCTCAG GGGTCTCCTGTGTTGACATGTTATGTCAGGTTAAGCCATTTTAGCATTCTTAGTTTTCTG

8680 CTTGAGACCCACATGTGAAAACTGTCAGTCTGTTATCACTTAAGACAGAAGAAAATTGCC CTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGACAGCTTTCCTGCCATGTGGCA CACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCCCTTGAGCTAGAAGTGTTGAC TGTCATGGGAGGTGCATGAATTCGTACTGCAGAGTGGCTGCTCAGGGGTCTCCTGTGTTG [A,G]

> CATGTTATGTCAGGTTAAGCCATTTTAGCATTCTTAGTTTTCTGAGGAAACTCCACAGAA AGTTTTGCTTATTTCTTAGAAGTAAGGACAGATACCGGTTTCTCACCTGTCCTCTGCTC CTGTAGGCACATTGAGGATAAGTCCACCGTGTTTTGGGACTGCGCTCAACTATGTGTCTCT CAGAATTCTGGGTGTTGGGCCTGACGATCCTGACCTGGTACGAGCCCGGAACATTCTTCA CAAGAAAGGTACGGCATGTGCAGCATGTGCTGGGCCAGGGGTTCGTGTCAACTCGATAAT

8700 ACTGTCAGTCTGTTATCACTTAAGACAGAAGAAAATTGCCCTTGACTCTGGGCTGGCAGC AGGTGGAGACAAGGCCTGACAGCTTTCCTGCCATGTGGCACACACTTTGGGAGCAGAGCC ATAGCCCAAAGTGGACCGCCCTTGAGCTAGAAGTGTTGACTCAGGCGTGGGAAGGTGTAG AGCAGGCGGTCACGGTGAGGAAGGAGTGGGGGGCTCAGTTGTCATGGGAGGTGCATGAA TTCGTACTGCAGAGTGGCTCAGGGGTCTCCTGTGTTGACATGTTATGTCAGGTTAAG

> CATTTTAGCATTCTTAGTTTTCTGAGGAAACTCCACAGAAAGTTTTGCTTTATTTCTTAG AAGTAAGGACAGATACCGGTTTCTCACCTGTCCTCTGCTCCTGTAGGCACATTGAGGATA AGTCCACCGTGTTTGGGACTGCGCTCAACTATGTGTCTCTCAGAATTCTGGGTGTTGGGC CTGACGATCCTGACCTGGTACGAGCCCGGAACATTCTTCACAAGAAAGGTACGGCATGTG CAGCATGTGCTGGGCCAGGGGTTCGTGTCAACTCGATAATGAGCTCTCACAAACGAGATA

8996 TAAGCCATTTTAGCATTCTTAGTTTTCTGAGGAAACTCCACAGAAAGTTTTGCTTTATTT CTTAGAAGTAAGGACAGATACCGGTTTCTCACCTGTCCTCTGCTCCTGTAGGCACATTGA GGATAAGTCCACCGTGTTTGGGACTGCGCTCAACTATGTGTCTCTCAGAATTCTGGGTGT TGGGCCTGACGATCCTGGTACGAGCCCGGAACATTCTTCACAAGAAAGGTACGGC ATGTGCAGCATGTGCTGGGCCAGGGGTTCGTGTCAACTCGATAATGAGCTCTCACAAACG [A.Cl

> GATACAGAAAGATGCACTTGCAGCTGAAACAGTGGGCAAAAGCACATGAGCAGGGAATTT GTCAAAGCAGAAGTAGGCAGACACTGTTTAACCTAGGCATCATTTTTTAAAAAAGCAAAT TAAGAGCCAGGCACAGTGAGTGGCTCACGCCTGCAATTCCAGCACTTTGGGAGACTGAGG TAGAAGGACCACTTCAACCTAAGAGTTCGAGGCCAGCCTGGGCAACATAGTGAGACCTGG TCTCTACAAAAACAATAAAATATTAGCCAGGTGTGATGATATGCACCTGTAGTCTCAGCT

10590 CATGAGATCCTGCCTTCTTTCTTGGTGAGCTTGTCACTATTGTCCTCAGTTCACTGTCAG CCTTTGGTGTCGTTGATGCTGCGTCCCCAAGGCTGCTGTCCGGTTCCCACCACACTCCTG GCGCCTGCTGAAGGAACGTGTTTAGGCTGCACTTTGCCTAGTAGCTTTGTGGGTCT TTATTGACTTTTGCATACCTTTTGGGGTTTTGGAGCAGGGACTCCTCAGAAGCATGTTTAG ATGGTGTGGCTGTGCCAGGACTGCTGCTGCAAGTGGCTCTGGCATGGGGCCAGCGTGC

> GGAGCTACTCTGGAGTCTAGGGTCGTCTTTGTTCCCATACAGGACCAGTCTGCCAAGTGG AGATGACACAGACTGGGGCAGCTCAGGCTTGGCTCAGAGGGCGAGGCTGAGTGTGCGCTG TCACTTCCCCACCTTGCCTTCTCCAGGCGCATGTGCACCTGGGCCCCTCGCTCACCTGAG GGGGTTGCAAACACCTCTCCTGGGGCTGGACACACACCCCCAGGAAAGCCACTGGTTC

> > FIGURE 3R

11090 CTTCCCAGGTAGCTGTCTTCATGTGCTCCTTCCTGGGGCCAGGGGTTGCAAACACCTCTC
CTGGGGCTGGACACACACACTCCCAGGAAAGCCACTGGTTCCACCTAGGGGGCCGTGTAT
CCAGGCAAGTTCTCAGCACTCTGGAACCTGCTTCGCACATGGGGGTCGCAAGATCCACAT
GAGGCTGCCCTTGCCTCATGGAGAGGGGCACACGTGACTCCCAGAGGGTGAAGCTTCCCA
GCTAGAGGCAGTGCAGACTTTGCTGACAGGAAGCAGATGACGTGGCCTATTCTCCCC
[G,C]

12591 GTGCTGGGAGCCATGAGCCACTGCTCCCGGCCTTATGTGGTGTCTTTAACCAGTGTCTTG
TAACATTTTATGGCTATCTATTGAAAGCAGTGGACATCTCCCCAGAAAACACTCGTGCAT
ATGAGTTTACCCCGTTATGCATTTTGGGAAGTGAGACCCTGGAACCACAGAGCCCCTG
CTGGCTTCCTTGAGTGTTGTGGGAACCCTGGTGGGGGTTGCCCCTACAGAGCTATCATCA
GGGCTGGGGGGGTCCCTTGTGTTAGATGACTTTGGTGCGGGGGTTGGGGGGGTCA

[C, \(\lambda\)]

TTTTTTTTTTTTGAGACAGAGTCTCTCGCTCTGTCACCAGGCTGTGCAGTGGCACAA
TCTCGGCTCACTGCAACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAG
TAGCTGGGACTAGAGGCACACACCACCATGCCTGGCTTATTTTTTGTATTTTTAGTAGAGA
TGGGGTTTCGCCATGTTGGTCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCCACCAG
CCTCGGCCTCCCAAAGTGCTAGGGTTACAGGCGTGAGCCACCGTGCCCCTCCTAAAGTTT

14746 CATCCTATAATAAACAGTGAGCAAGCTCTGCCCAGAGGGGACTTGTGCTATGGGACAGTC
AGTAGCTGTAGCCCAGGGTTCCTGGGGGGGACTTCCAGGACTCAAGGGATGCAGGAGGCA
GATGTGCACTGTGTCCTCTGGAAGCAGGCCTGAGGCGAGGTTTGAGGTGCAGGATGTTTA
TCAGGCCTGCCATGGGGAAGAAGAGGGGGCAGAGGGAAATGAGCTTCTGGGCAGACC
TGGGACTCATGGAGCTGGGGAGCTCCTCAGAGCGGTCCTCCCATAGGGGGCCTTCATGTG
[C,G]

CCTCGGGGTCAGTTGCTGGAGGGACCCCCACCCAGGAAGGGACTGGCCCAGGGCCCTGAG GGCGGATGGTGGGAGGCCACCCCTCCTGGTTTGAGCCAGGCCTACCAGGTGCTCCCAGGC CCCAAGGCTCAGACACTGCCCCTACCAGGAGCTCTATGTGGAGGACTTCGCCAGCATTGA CTGGCTGGCGCAGAGGAACAACGTGGCCCCCGACGAGCTGTACACGCCGCACAGCTGGCT GCTCCGCGTGGTATATGGTGAGCGCCTCCTGAGGGGCCGGCAGGGCAGCCCAGGGTCAGG

GTGCTCCCAGGCCCCAAGGCTCAGACACTGCCCCTACCAGGAGCTCTATGTGGAGGACTTCGCCAGCATTGACTGGCGCAGAGGAACAACGTGGCCCCGACGAGCTGTACACGCC

TTCCGTCCCCACCGGCTCTTGTCCTCAGTGTGCCTGGACACTCTCCTAGAGGCCCCTCC
CTGAGATCTTGCTGGCTAGCTGGCTGGGAGGGGTGCTTTTTCCTCACTTGGTTCCC
TCTCCCCAAACAGTTCATCATTCGCCATTCTCCCGTGGGGTTTAGACATGCCCAGGGTGG
GTGGGAGTAGCAGGTGCCACTCCTGATTCCTCCTGCCTAGGTAGCACTTGGAGCTCTCA
CCTCTGTGGGGCCTGCAGGGGTCCAGGTGGCCAGTTCAGTGACCTTAGAGGGTGCAAT
[C,T]

GTGGAGTGCTCCTTCTCACAGCCTAAGGCAGGCTGTGGCCTTGGCCGACACTGCCTC
TGTCTGAGTTGGGTCCTGGGGGACACAGTTGTTGCCCATCCTCGCTCAGGAAATGCCTGTT
AGAGCAGAAGGCCCCTGTCCTGGCCCTGAGTGATCTGCACGGCACTTTATGCCTGGGGGC
TGCTGTGGATCTGGACGAGACCTTGTCCCTGGAGGCTGCTGTGGGTCTGGAGCCGAGCCT
TGACAGGGCTGTCTCTCCTGCAGATCTCGAAAACCATCAACATGCTTGTGCGCTGGTATG

GGACGGCCCGCCTCCACTGCCTTCCAGGAGCATGTCTCCAGAATCCCGGACTATCTCTG
GTGAGTGTGGCTGGGATATGCTGGCGGGGCCTCTCACGAAGACTGGATCTGAGCCCCAGC
TGCATCCCAGTGAGGGGCCCCCACGGTGCCATCTGGGAATACTGCCAGGGAATACCTCC
AGGAACCAGCAGTGTCAGGGCTTGTGGAAGCCACTGAGGGTTGTCTTTGAATTGGAAGAT
TTGCCACCCAGTGGAAGTGTGGGGTGTTCCCAGAAGGTAGAGTGAGGAAGGGGGTGGTAG

19359 CCACACACCCCCTGCCCAGTCCCCATGTCTGTCTGGTCAGTGCCCAGCTCTGTCTCA
CTAGGGTTTGGTCACCGGCCCTTTGAACTGAGACCAGGCTGTGTACCTGTGAGCCAGCT
CGGGGTGAGATTTGAGGTGGAGCCTTCCCAGCCCTGTGCAGAATTCCCATCACCTCCAGG
TGTACTCAGAAATGGGGATCATTGGCCAGGTGCGGTGGCTCACGCCTGTAATCCCTACAC
TTTGGGAGGCCAAGGTGGGCGGATCACAAGGTCAGGAGATAGAGACCATCCTGGCTAACA
[C,T]

FIGURE 3T

> GACGTGTGTCTGCCTGCAGGGCTCAGCCTTCTCTGAGGCCCTTGTCAGCCATGAGGGGTG CCCAGGGCTCAGAGCCTGAGGCTTGGCTGGGTGGGAGCCCCACACCTGGCCCT CAGGCGCCCATTGGATCCTGGAGGCAGTGGCTGGGAGTGGGAGGGGTGCATCTGCTGCT GTAACACCATCCTTTGTGTGTAGGGCACCAACGGCTCACAGATCTGGGACACCGCATTCG CCATCCAGGCTCTGCTTGAGGTTCGTGGCTCCTTCTCTTTTTCTCAGCCTCAGCTGACCTT

20054 GCCTGCAGGGCTCAGCCTTCTCTGAGGCCCTTGTCAGCCATGAGGGGTGCCCAGGGCTCA
GAGCCTGAGGCTGAGCGTTGGCTGGGTGGAGCCCCCACACCTGGCCCTCAGGCGCCCAT
TGGATCCTGGAGGCAGTGGGAGTGGGAGGGGCTGCATCTGCTGCTGTAACACCATC
CTTTGTGTGTAGGGCACCAACGGCTCACAGATCTGGGACACCGCATTCGCCATCCAGGCT
CTGCTTGAGGTTCGTGGCTCCTTCTCTTTTCTCAGCCTCAGCTGACCTTCCTGTGCACGT
[A,G]

> AACTGGAACTGTTTGTTATGGGCATTCTCGAGCCAGTACTGGAGAAAAACGAGAGTGGAT TTTTATGCCGGTGGGAATGAGGTAGGTGGGATTCTGAAGGTGTTTCTGGAGAGCCCTGAG GGCTGGGCCACGCAAAGGGCCTGCCTACACAGGGTGCTGGAGACCCTCTGGGCATGGATG CTGGCCAGGCAGGGGGGTGCTGGCATCCATAAATGGTCTCCTGCGCCCTTCCATCTTCAG TCATATCTCATGGACTTTTGCTGTTTTTGTCTTTAAAGGTAAGTGCAGCAGGAGACCCTGG

> TCTCTGAGGCCTGCAGGTGCTGGGGGTGCTGGCAGTTTCTGCGTCCTGCTCATGTTGGA GCCACTGTGTGCAAGGGCCAGGCACGGGCAGGGCTGTGTACCCTGAGCTGCACAGCCTA CACGGCACCTCCATGTCTCTGAAGCACCTTCTGCCCATGGAGGTGACGCCAGCCTGTGGA CTTGCCCTCCTGAGACTGTTTGCAGCAAAAGCCCCGGTCCCTCCTGCCAGATCAGCTGCC CACAGACCCTGCCCGAGCCCATAGTTTGACCTCAGTGTCTCTCACACGTGCCTGCACCCC

21894 GCCCATAGTTTGACCTCAGTGTCTCTCACACGTGCCTGCACCCCAGTCTGCAGCCACAGT
CATCCCATACATGCGCCCCAACCTCCCGTGTCTCCCACACCCTGTCCCGGCCACGGCCTC
AGCCAGTGTCCCTCTGCCTGGAACCGCTGCCCCCAGCCCGTCTCCCTTCCTGTCTCAGCTC
TCACTAGGACATTGTTCTGCAGGGCTTCTGGGTCTTCCTGGCCTCTGTGTGGCCAAGGCT
GGCACCCATCTTGGGCTCAAGCAGAGGAGGGGCATTGTCCTGCTGTGCCTGGCCCAATGG

GGCCTGCTCCTGCCTCCTGCCCAGGACTTGCTCTGGGTGATGGGGACTTGGGGA GGCTGACTGAACCCTACGGCACTCCAGGCCTCTTCCCTTCTCACTGAGGTGAGAGAGGCA GCCAGAAGCTGAGGTTGTTCAGGAGGCATTGGGGGCGCCTGGCACAGAGCACACCCGCAG

FIGURE 3U

AGACCTGGGCCCCTCCCTGCCTTCTGGCCGGTGGGGAGATCACAGGGGAGTCAGGTGCTGACTCCCAGTCCCGTCTGGGCTGGTTTGAGCCCTCGCTGGCCAGTCACGTTTCCCAGCAG

TGAGAACTGGGGTGGACACCCCCAGCCTGGAGTCATGGCTTGTGCTCTGCAGGGTGGC
TTCTCCTTCAGTACGCTGGACTGCGGCTGGATCGTTTCTGACTGCACGGCTGAGGCCTTG
AAGGCTGTGCTCCTGCAGGAGAAGTGTCCCCATGTCACCGAGCACATCCCCAGAGAA
CGGCTCTGCGATGCTGTGGCTGTGGTAAGGCTGTGGTCCCAGCAGCCCCGTCCATACCTC
GTGTCCTGCAGATGAGCTGCGTGCTCACTTCCACTCCTGTGGGCTCCAGCCCAGCACACA
[G,T]

TCCGGCCAGGCCGTAGGAGCTTGTCCTTGGATGGTGTCTATATGTGGAGAACTGTGAGCT CTGGCTGGACCCCTAGGGGCCTTGCTGGGCTGTGCACAGGGCCCTGCACTGCGGAGCT GGTGTCCAGCCCACCGATACTTGGGGGAGCCGGCGTGGCCCCCAAGGTTTCTCTCT GGTGGTTTCCACTGGGTGTCTGAAGAGGGAATTTGTTGGTGTTTTGGTGCCACATC CTTTCAGCACATCTGGCTTTTGTGTGTGTTTTCCCAGTGGAGACCCTGCCCTTTTCTGGCA

> GGCCATGTGCTGCTGCGGCATGAGGTGGGCGTGAGTTGTCCTCAGCCACATTTAGAGA ATTGGCCTTTTAAAAAATAGATCATCTTTTAAAAATCACTGTAATAAAAGTAAAGCAGGT TCTTTGCAAACAAGACTTGCAAAATACAGAGAAGCGCAAAGAAGAAGCTAAGTCGCCCCT CCTCGCCCCTGAAGGAGAATCTGCTGTTGCTGTTTGGTCTCCACATTTCCATGGCGGCTT GCTGCCCCTTTCACGCCTGGCCCACTTTGTGCCTGTGAGGTTTCTAAAAGCCCCACCCT

27332 TTGGCCATGTGCTCTGCGGCATGAGGTGGGCGTGAGTTGTCCTCAGCCACATTTAGA
GAATTGGCCTTTTAAAAAATAGATCATCTTTTAAAAAATCACTGTAATAAAAGTAAAGCAG
GTTCTTTGCAAACAAGACTTGCAAAATACAGAGAAGCGCAAAGAAGAAGCTAAGTCGCCC
CTCCTCGCCCCTGAAGGAGAATCTGCTGTTGCTGTTTGGTCTCCACATTTCCATGGCGGC
TTGCTGCCCCTTTCACGCCTGGCCCACTTTGTGCCTGGTGAGGTTTCTAAAAGCCCCACC
[C,A]

TTGAGCGCGCTCCTCCAGCACGAGCAGTAATGGCACAGGTGTTGTGTCATTTTACTCAGT AGCCTCTGGGTTATTTTCAGTTTTCCCTTGTTGTTTTTTTAGCTTTTTCCCCATTTTAACCT TAACTGGTATTTTCTTGTTAAATATTTATTCATGACCATTATTATTCCCTAGAGCCACAT GGCTTGGGGTCCACCTGGGTCCGCCCCCATCCCTGCCCTTCTGGCTGTCTGACCT GGCCTGGTGACTTCTCTCTCTCTCTCTCTCTCTCCTGACTGGCCAAGAGTACAG

> > FIGURE 3V

27625 CCCCACCTTGAGCGCGCTCCTCCAGCAGGAGCAGTAATGGCACAGGTGTTGTGTCATTT TACTCAGTAGCCTCTGGGTTATTTTTCAGTTTTCCCTTGTTGTTTTTTAGCTTTTCCCCAT TTTAACCTTAACTGGTATTTTCTTGTTAAATATTTATTCATGACCATTATTATTCCCTAG AGCCACATGGCTTGGGGTCCACCTGCCTGGGTCCGCCCCCATCCCTGCCCCTTCTGGCTG

> AGTACAGCCTCACAGAGTGGTGGGGATTGTGTGAGATGCCACAGGGAAGCACATGTCAGTT GTTGTCACTGTGTAGAACAATGAGTCCCGGATGTGGCCCGCAGGGGAGCAATGGTGACTT ${\tt AATCGCGGGCTTCCTCTGCATTTCTTTGGTGACTTCCAAGCTAGAACATTCTTTTTTTGT}$ TTATTTGTTTGAAGCAGGGTCTCACTCTGTTACCTAGGCTGGAGTGCAGTAGCAAAATCA TGGCTCACCACAGTCTCAAACTTCCGGGCTCAAGCAATCCTCCCACCTCAGCCTCCTGAG

27736 ATTCCCTAGAGCCACATGGCTTGGGGTCCACCTGCCTGGGTCCGCCCCATCCCTGCCCC AGTGGGCAAGAGTACAGCCTCACAGAGTGGTGGGGATTGTGAGATGCCACAGGGAAGCA CATGTCAGTTGTCACTGTGTAGAACAATGAGTCCCGGATGTGGCCCGCAGGGGAGCA

> TGGTGACTTAATCGCGGGCTTCCTCTGCATTTCTTTGGTGACTTCCAAGCTAGAACATTC TTTTTTTGTTTATTTGTTTGAAGCAGGGTCTCACTCTGTTACCTAGGCTGGAGTGCAGTA GCAAAATCATGGCTCACCACAGTCTCAAACTTCCGGGCTCAAGCAATCCTCCCACCTCAG ${\tt CCTCCTGAGTAGCTGGGACTACAGGTGCATACCATCACCTGTGGCTAATTTTTTAAATGT}$ TTTGTATTTTTAAATGTTGCTCAGGCTGGTCTTGAACTGCTGGGCTCAAGCAATCCTCC

> TACGCAATTGATTTTGATACTGATCTCATAGCTAGACAATTTTGCTAAACTTTTAAAAAA ATTTATGTACTTTATCTTTTATAGCAGCTTTAAATTTACAGAAAATTTGAGTGGAAGATG CAGTGTTCCCATAAAGCCGCTAACTCCTCGCACCTTCCCTCAAGTTTCCCCAGTACTAAC ATCTTGCATTCAAGTGGTGCGTTTGCAACATTCATAAATTATTGTCCAGAGTCCATT ${\tt GTTTACATTCAGCTTCCTCTTCATGTTGTTCATTCTGTGGTTTCACAGATGTGTGATGCA}$

> GTGCCCACCACTGCAGTGTCACACAGGATCTCACTGCCCCGGAGTCCTCTGCGCTGTCCC CGCCTCCAGAACCCCTTAGTAGCAAACACTGATATTTTTACTGTCTCCATAGTTTTGCCT TTTCAGACTGACCTATTTCACTTAGTAAGAAGCATTTAAGATTCCTGAGTCTCTTTCTAT GGCTCAATAGCACATTCTTTTTAGTGCTGAATAATATTCCATTGTCTGGATGTACCACA

31172 ${\tt TCAATAGCACATTTCTTTTTAGTGCTGAATAATATTCCATTGTCTGGATGTACCACAGTT}$ TATTCATTCACCTACTAAGGTGAATGTCTTGCTTGCTTCCAAGTTTTTGGCAACTATGAAT AAAGTTGCTATCAATGTTAGCGTGCACATAAGTTTTCAGCTCATTTGGGTAAATGCCAAG AAGCATGATTGCGGGATCCTATGGTAAGAGTGTTTTAGTTCTGTAAGAAGCTGCCAAAC TGTATCTTAAGTGGCTGCACCATTTGCGTTTCCACCAGCAATGATGAGCGTTTTGTTGCT [C,T]

> ${\tt CACATCCTCACCAGCATTTGCTGTTGTGTTTTTGGGTTTTAGCCTTTCTAAGAGGTGTGTA}$ GTGGTATCTCCTTGTTTCAATTTGCAATTCCCTAATGACATTATGTTAAAATCTTGTCAT ATAGTTATTTGCCATCTGTGTATCTTTTCAGTGATGTGTCCTTTAAAGTCTTTGGCTCA TTTTTAAATTAAATTTCTTATTGTTGAGTTTTAGTTCTTCATATATTTTTGGCTGCCAGT CCTTTATCAGATATGTCTTTCGCAAATATTTTCTGCCTGTGTCTTGTCTTTTCATTCTAT

31433 ${\tt ATTTGCGTTTCCACCAGCAATGATGAGCGTTTTGTTGCTCCACATCCTCACCAGCATTTG}$ CTGTTGTGTTTTGGGTTTTAGCCTTTCTAAGAGGTGTGTAGTGGTATCTCCTTGTTTCAA TTTGCAATTCCCTAATGACATTATGTTAAAATCTTGTCATATAGTTATTTGCCATCTGTG TATCTTTTCAGTGATGTCCTTTAAAGTCTTTGGCTCATTTTTAAATTAAATTTTCTT ATTGTTGAGTTTTAGTTCTTCATATATTTTGGCTGCCAGTCCTTTATCAGATATGTCTTT [C,T]

> GCAAATATTTTCTGCCTGTGTCTTGTCTTTTCATTCTATTAACAGTATCTTTTTGCAGAGC CAGTTTTCATTTCAAGGAAGTCCAGCTTATCAATGTTCTCTTTCATGTATCATGTTTTTG GTGTTGTATCTAAAAAGTTACTGCCAAGCCCAAGGGTACCTAGATTTTTTCCTGTGTTAT ATTCTAGGATTTTAAAGTTTTGCATTTTACATCTAGGTCCATGATTCATTTTGAGTTAA

32660 CTCCTGGGCTTAAGGAATCCTCCTGTCTCAGCCTCCTGAGCAGCTAGGACCACAGGCATG TGCCACTACGTTCAGCTAATTTTTCAATTTTTTTTGTAGAGATGGGATCTTGCTCTGTTGC CCAGGCTGGTCTCAAACTCCCGTCTGCTTTGAGATGATTATATATTTTGTGTCCTTTGTTA

FIGURE 3W

32981

TCTCTGTCTCCCAGGCTGGAGTCCAGTGGCACAATCTCAGCTCACCGCAAGCTCTGCCTC
CCGGATTCACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCTGT
CATCATGCCCAGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTAGCCA
GGGTGGTCTCAATCTCCTGACCTCGTGATCTGCCCACCTCGATCTCCCAAAGTGCTGGGA
TTACAAGGCGTGAGCCACTGCGCCCGGCAGCAGTTTCTCAGTTTTAATTTGGAGTTTTGC
[A,C]

TCTGTGTTCATGAGTGAGCCTGAAATTTTCACTTTTCCATATCTTATTTCTCTGGGTTCC
TAGAATGAGCTAGAGAGTGTTCCTCCTTTCTGTTCTCTGGAAGAGTTTGTGTGAGAATTAG
AATGAGTGTGTCTGATAATTTAGTTGCATTCATTTATAAAATTCCTAGGCCTAGAGTTTT
TTTTCTGGGAAAAGTTTACATTTTGACTCATTTTTTTTAGTAGTTTTAGGACTGTTTAGGT
TCTCTATTTCTTGATTGAGCCAGTTTTGATAAGTTAATCTTTCTAATTTGTAGATATTTT

33557

GGGGTCTCGCCTGAGCTTCCAGTGAGGAAGGATCTGCCTCTGAGCACACAGGGTCCTCGG CACGATCCCATTCCTCAGCTGGAAGCTGCCGACTGCCGTCTGCTGCGGGGCCTCTCTAGA TGGCATCTTCACAAAAGCGAGAAGGGAGAGTTGGTAGAGGGAGTCTGCTAGCACCATGGG AGTCGCGGTCACACAGACCTCGGTCCCAGGACCCGCACCCATCAACCCTGCCGTGATCTG CTGGTTAAAGACAAGTCCCACGTCCCACAGGGTGACACTGGAGTAGACACTTCGCTCTGG

33652

-5

34390

34399

34989

35067

35495

CAGTCTTCCTACCTCGGCCTTCCAAAGTGCTGGGGTTACAGGCATGAGCCAATGTGCCTG
GCCTGTTTTTAATATTTTTAAACAGTGAGATAAGATCCCCGGTTGAAATGAAGATGTTTC
CCTGGTCCCACAGCTCTCTGGAGCTTCCTGACATGTATGCTGGAGGGACGCTTCTGGTCT
CCGGCCCCTCCAGGCATACAGATGCCTCCCAACCCTGAGTAGGAAGATTAGGGTCCACGG
CCTCGCTGGAGCGGGTTAGAAGGCAGGAGATCTCCGGTCCCAGCCGTGTCTCCAGCCGCC
[G,A]

36001

GGCAGGAGTATCTGTTCCCAGTTCACATCTGCAAAAGTCAAGCTCGGGTTTCAGTAGTGG CCCATGGCCCTTAGGTAGGGTGGCCCCATCGTGCAGGCTCCTCCCCGTACCCCAAGGCAG CCTGCTGGGGTGAGAAGCCAGGGGTCTGGGACCTTCCTTGGTGTATGGTGTCTCCTGTC TCTGGTCTTTGCAGGACTGCCTGTGCAGAGGTCTCCCGGGCCTGTGACTTCCTGCTGTCC CGGCAGATGGCAGACGGAGGCTGGGGGGAGGACTTTGAGTCCTGCGAGGAGCGGCGTTAT [T,G]

38948

ACAGCTCCCCAATGGCGACTGGCCGCAGGTATGCCGCCAGGGACCTGAGCGCACAAGGCC
CAGCACTGACCTCCAGCGTGCATGGCTGTTTCCACGTCCCCTGCTCTGTGTCCTTTTTG
GGGTACTTTGGACACTTGGGAGGCGTCACCTCTGCCAGTGAATGCCACAGTTGGTGGCAG
GTCTGTGGCAGGTGGTCGGGTCCTAAAGTCCAGATCTTGCTGTTTTCAAGTGATGCTC
TGGGTGGGGGAGGAGCTGGATGGGAGAAGCCAGTGGGCGGAAGCCTTTTTGCTGCAGGA

AGACCCTCCCACTCCAGATGACCTAGTGGCCCCTCACTGAGCCAGAAGTCCCTGTGGTGT GGGTGTCATGAGGTCATGTGAGGCCAACCGCCCTCCCCTGGGATGAGGCTGAGTTGGTGG AAGCTGATGTGGTTGTGAGGGCTGGTGACCCTGGCTTAGGGTTTGCTGCAGGGCGGGA

40794 CAGTCTCATGCCCAGGTGGTGCTCTGGGCTGGAGCGAGGGCCAGGTTTTGGGCCGAGGC
TTCCCCAGGCAATCCTGTGAGCTCCCTTCTAGCCTCTGACCCAGTCTGGTCTGGCTTGCA
TGGATGTAGGGCTTGGGGTAGGAGTTCAGGTCCTGGCTTTGCCTTTGCCTGATGTGGAT
GAGCAGCTCACATGCTCAGGGCCACCTGAGACTGTCACTGCTCTCCCCTGGCTACTGGGA
GGAGTCACTGAGAGCTTCGTTACCCCTGCTGCCTAGCCCAGGGCACACCCTATACCTCCT
[C,T]

ATCTGCTCTTCCCCTCCCTGCCGCCTTCTGGGCAGGTAGCAGTCCCTGGCCTCTCCCCCT GGCTGATCACTCTCCCTCAGGCAGTGGAGATCTGCGTCTGGACACCCTCAGATCCTGTCA TTGCCTGCCCAGAGTCCTTCAGGGGCACCCCTCTGCCTTGGTGTGCGGTCCAGGGCTCTC ACCCAGGTGCCGCACCCTCTGGGGTCTTCTGTCCAGCTCCCTTGCCCCATGTGCTGTCAC TGACTCTCCTTGGGACTCGCCTGCTGAGAGCCCTGCAGGGCTTGGTCAGCTGCCTG

40961 GCCTGATGTGGATGAGCAGCTCACATGCTCAGGGCCACCTGAGACTGTCACTGCTCTCCC
CTGGCTACTGGGAGGAGTCACTGAGAGCTTCGTTACCCCTGCTGCCTTGCCCAGGGCACA
CCCTATACCTCCTCATCTGCTCTTCCCCTCCCTGCCGCCTTCTGGGCAGGTAGCAGTCCC
TGGCCTCTCCCCCTGGCTGATCACTCTCCCTCAGGCAGTTCTGCGTCTGGACACC
CTCAGATCCTGTCATTGCCTGCCCAGAGTCCTTCAGGGGCACCCCTCTGCCTTGGTGTGC
[A, G]

AGGGAAACAGATATTTTAAGAGATAATAGCCTATTTTAATATGTTTTAAAGGCC
ATAAGCATATCCAGGAAGATAAATAAACGTGATACAATGTCCACATAGGAGGAACTTTCT
TTCACTGCATTGTTTTCCTTCACAGTGGCCTTCAAGTCACAGGACGCAGCGATTCCCTGC
CCTCTTCGGTGTTATTACACAGGCAGGACTTCAGTGTCAGTATCCCTGCCTTCAGTCTTC
TTTAGAAATCACATCTGTGTTCAATCCATTGTTTAGAGGGAGTGTATTTTTCCTGTTCCA
[C,T]

FIGURE 3Z